

## FIGURE 1

CCAGGTCCAAC TGCACCTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCT  
CGACCTCGACCCAC CGCGTCCGCCAAGCTGGCCCTGCACGGCTGCAAGGGAGGCTCCTGTGGA  
CAGGCCAGGCAGGTGGCCTCAGGAGGTGCCTCAGGCCAGTGGCCTGAGGCCAGC  
AAGGGCTAGGGTCCATCTCCAGTCCCAGGACACAGCAGGCCACC ATGCCACGCCCTGGC  
TCCAGCAGCATCAGCAGCCCCAGGACCGGGGAGGCACAGGTGGCCCCACCACCCGGAGG  
AGCAGCTCCTGCCCTGTCCGGGGTGACTGATTCTCCTCCGCCAGGCCACCCAGAGGAGA  
AGGCCACCCCGCTGGAGGCACAGGCCATGAGGGCTCTCAGGAGGTGCTGCTGATGTGGCT  
TCTGGTGTGGCAGTGGCGGCACAGAGCACGCCAACCGCCGGCGTTAGGGTGTGTGCT  
GTCCCGGGCTCACGGGACCCCTGTCTCCGAGTCGTTGTGCAGCGTGTGTACCAGCCCTTC  
TCACCACCTGCGACGGCACCGGCCCTGCAGCACCTACCGAACCAATTATAGGACCGCCTAC  
CGCCGCAGCCCTGGGCTGGCCCTGCCAGGCCTCGCTACCGTGCTGCCCGCTGGAAGAG  
GACCAGCGGGCTTCCTGGGGCTGTGGAGCAGCAATATGCCAGGCCATGCCGAAACGGAG  
GGAGCTGTGTCCAGCCTGGCCCTGCCCTGCAGGATGGCGGGGTGACACTTGCCAG  
TCAGATGTGGATGAATGCAGTGCTAGGAGGGCGGCTGTCCCCAGCGCTGCATCAACACCGC  
CGGCAGTTACTGGTGCCAGTGTGGAGGGCACAGCCTGTCTGCAGACGGTACACTCTGTG  
TGCCCAAGGGAGGGCCCCCAAGGTGGCCCCAACCCGACAGGAGTGGACAGTGCAATGAAG  
GAAGAAGTGCAGAGGCTGCAGTCCAGGGTGGACCTGCTGGAGGAGAAGCTGCAGCTGGTGT  
GGCCCCACTGCACAGCCTGGCCTCGCAGGCACTGGAGCATGGCTCCGGACCCGGCAGCC  
TCCTGGTGCACTCCTCCAGCAGCTGGCCGATCGACTCCCTGAGCGAGCAGATTCCCTTC  
CTGGAGGAGCAGCTGGGTCTGCTCCTGCAAGAAAGACTCGTGACTGCCAGCGCCCCAGG  
CTGGACTGAGCCCCCTCACGCCCTGCAGCCTGCCATGCCAACATGCTGGGGTC  
CAGAAGCCACCTGGGGTGAUTGAGCGGAAGGCCAGGCAGGGCTTCCTCTTTCTCCTC  
CCCTTCCCTGGGAGGGTCCCCAGACCCCTGGCATGGATGGCTGGGATTTTTGTGAAT  
CCACCCCTGGCTACCCCCACCCCTGGTTACCCCAACGGCATCCCAAGGCCAGGTGGCCCTCA  
GCTGAGGGAAGGTACGAGTTCCCTGCTGGAGCCTGGGACCCATGGCACAGGCCAGGCAGCC  
CGGAGGCTGGTGGGCCTCAGTGGGGCTGCTGCCTGACCCCCAGCACAATAAAATGAAA  
CGTAAAAAAAAAAAAAAAAGGGCGGCCGCGACTCT  
AGAGTCGACCTGCAGAAGCTTGGCCCATGGCCAAC TTGTTATTGAGCTTATAATGGT  
TACAAAT

## **FIGURE 2**

MTDSPPPGHPEEKATPPGGTGHEGLSGGAADVASGVGSGRHRARLPARPLGCVLSRAHDPV  
SESFVQRVYQPFLTTCGHRACSTYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGAC  
GAAICQPPCRNGGSCVQPGRCRCPAGWRGDTCQSDVDECSARRGGCPQRCINTAGSYWCQCW  
EGHSLSAADGTLCPKGPPRVAPNPTGVDSAMKEEVQRLQSRVDLLEEKLQLVLAPLHSLAS  
QALEHGLPDPGSLLVHSFQQLGRIDSLSEQISFLEEQLGSCSCKKDS

**Signal sequence:**

amino acids 1-19

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 93-97, 270-274

**N-myristoylation sites.**

amino acids 19-25, 78-84, 97-103, 100-106, 103-109, 157-163,  
191-197, 265-271

**Amidation site.**

amino acids 26-30

**Aspartic acid and asparagine hydroxylation site.**

amino acids 152-164

**Cell attachment sequence.**

amino acids 130-133

**EGF-like domain cysteine pattern signature.**

amino acids 123-135

### **FIGURE 3**

CGCTCGCCCCGTCGCCCTCGCCTCCCCGAGAGTCCCCTCGCGGCAGCAGATGTGTGTGGG  
GTCAGCCCACGGCGGGACTATGGTGAAATTCCCGGCGCTCACGCACTACTGGCCCTGATC  
CGGTTCTTGGTGCCTGGCATACCAACATAGCCATCGACTTCGGGGAGCAGGCCCTGAA  
CCGGGGCATTGCTGCTGCAAGGAGGATGCAGTCGAGATGCTGGCCAGCTACGGGCTGGCGT  
ACTCCCTCATGAAGTTCTCACGGGTCCATGAGTGAECTCAAAAATGTGGGCTGGTGT  
GTGAACAGCAAGAGAGACAGGACAAAGCCGTCTGTGTATGGTGGTGGCAGGGGCATCGC  
TGCCGTCTTCACACACTGATAGCTTATAGTGTAGTTAGGATACTACATTATCAATAAACTGC  
ACCATGTGGACGAGTCGGTGGGAGCAAGACGAGAAGGGCCTCCTGTACCTCGCCCTT  
CCTTCATGGACGCAATGGCATGGACCAGTGGCATTCTTAAACACAATACAGTT  
CCTGGTGGGATGTGCCTCAATCTCAGATGTAGCTCAGGTTGTTTGAGCCATTTGC  
TTCACAGTCACCTGGAATGCCGGAGGCCCTGCTCATCCGATCCTCTCCTGTACATGGC  
GCACTTGTGCGCTGCACCACCCCTGCGCTGGCTACTACAAGAACATTACAGACATCATCCC  
TGACAGAAGTGGCCGGAGCTGGGGAGATGCAACAATAAGAAAGATGCTGAGCTCTGGT  
GCCCTTGGCTTAATTCTGGCCACACAGAGAACAGTGGCCTATTGTCAACCTCTTGTT  
TCCCGGGACCTTGGTGGCAGTTCTGCAGCCACAGAGGAGTGGCATTGACAGCCACATA  
CCCTGTGGGTACATGCCATACGGCTGGTGACGGAAATCCGTGTGTATCCTGCTTTCG  
ACAAGAATAACCCACAGCAACAAACTGGTGAGCACGAGCAACACAGTCACGGCAGCCCACATC  
AAGAAGTTCACCTCGTCTGCATGGCTCTGTCACTCACGCTCTGTTGTATGTTGGAC  
ACCCAACGTGTCTGAGAAAATCTTGATAGACATCATGGAGTGGACTTTGCCTTGAGAAC  
TCTGTGTTGTCCTTGCAGATCTCCTCTCCAGTCCAGTCACAGTGAGGGCGCAT  
CTCACCGGGTGGCTGATGACACTGAAGAAAACCTTCGTCCTGCCCTCAGCTCTGCTGCG  
GATCATCGTCCTCATGCCAGCCTCGTGGCTCACCTACCTGGGGTGACGGTGCACGGCGACCC  
TGGCGTGGGCTCCCTCTGGCGGGCTTGTGGAGAACATCCACCATGGTCGCCATCGCTGCG  
TGCTATGTCTACCGGAAGCAGAAAAAGAAGATGGAGAACATGAGTCGGCCACGGAGGGGAAGA  
CTCTGCCATGACAGACATGCCCTCGACAGAGGGAGGTGACAGACATCGTGGAAATGAGAGAGG  
AGAATGAATAAGGCACGGACGCCATGGGACTGCAGGGACGGTCAGTCAGGATGACACTTC  
GGCATCATCTTCCCTCTCCATCGTATTTGTTCCCTTTTTGTTGTTGGTAAT  
GAAAGAGGCCTTGATTTAAAGGTTCTGTCATTCTCTAGCATACTGGGTATGCTCACACT  
GACGGGGGACCTAGTGAATGGTCTTACTGTTGCTATGAAAAACAAACAAACTGAC  
TTCATACCCCTGCCTCACGAAAACCAAAGACACAGCTGCCTCACGGTTGACGTTGTGTC  
TCCTCCCTGGACAATCTCCTCTGGAACCAAAGGACTGCAGCTGTCATCGCGCTCGGT  
CACCTGCACAGCAGGCCACAGACTCTCCTGCCCCCTCATCGCTCTTAAGAACAG  
TTAAAACTCGGCTTCTTGATTTGCTTCCAGTCACATGGCGTACAAAGAGATGGAGGCC  
CGGTGGCCTCTTAAATTCCCTCTGCCACGGAGTCAGAACCATCTACTCCACACATGCAG  
GAGGCGGGTGGCACGCTGCAGCCGGAGTCCCCGTTCACACTGAGGAACGGAGACCTGTGAC  
CACAGCAGGCTGACAGATGGACAGAACTCCTGGTAGAAAGGTTGGTTGAAATGCCCGGG  
GGCAGCAAACGTGACATGGTGAATGATAGCATTCACTCTGCGTCTCCTAGATCTGAGCAA  
GCTGTCAGTTCTCACCCCCACCGTGTATACATGAGCTAACCTTTAAATTGTCAACAAA  
GCGCATCTCAGATTCCAGACCCCTGCCGATGACTTTCTGAAAGGCTGCTTCCCTCGC  
CTTCCCTGAAGGTCGCATTAGAGCGAGTCACATGGAGCATCCTAACCTTGCTATTAGTTT  
TACAGTGAACTGAAGCTTAAGTCTCATCCAGCATTCTAACATGCCAGGTTGCTGTAGGGTAAC  
TTTGAAGTAGATATATTACCTGGTTCTGCTATCCTTAGTCATAACTCTGCGGTACAGGTAA  
TTGAGAATGTACTACGGTACTTCCCTCCACACCACGATAAAAGCAAGACATTATAACG  
ATACCAAGACTCACTATGTGGTCTCCCTGAAATAACGCATTGAAATCCATGCAGTGCAGTA  
TATTTCTAAGTTGGAAAGCAGGTTTTCTTAAATTATAGACACGGTTCACT  
AAATTGATTAGTCAGAATTCTAGACTGAAAGAACCTAAACAAAAAAATATTAAAGATA  
TAAATATATGCTGTATATGTTATGTAATTATTTAGGCTATAACACATTCCATTTCGC  
ATTTCATAAAATGTCTCTAATACAAAAAA

## FIGURE 4

MVKFPALTHYWPLIRFLVPLGITNIAIDFGEQALNRGIAAVKEDAVEMLASYGLAYSLMKFF  
TGPMMSDFKNVGLVFVNNSKRDRTKAVLCMVVAGAIAAVFHTLIAYSDLGYYIINKLHHVDESV  
GSKTRRAFLYLAAPPFMDAMAWTAGILLKHYSFLVGCAISDVIAQVVFVAILLHSHLEC  
REPLLIPILSLYMGALVRCTTLCGYYKNIHDIIIPDRSGPELGGDATIRKMLSFWWPLALIL  
ATQRISRPIVNLFVSRLGGSSAATEAVAILTATYPVGHMPYGWLTEIRAVYPAFDKNNPSN  
KLVSTSNTVTAAHIKKFTFVCMALSLLCFVMFWTPNVSEKILIDIIGVDFAFELCVVPLR  
IFSFFPVPVTVRALGTGWLMTLKKTFLAPSSVLRIIVLIASLVLPYLGHGATLGVGSL  
AGFVGESTMVAIAACYVYRKQKKKMENESATEGEDSAMTDMPPTEEVDIVEMREENE

**Transmembrane domains:**

amino acids 86-106, 163-179, 191-205, 237-253, 327-343, 357-374,  
408-423, 431-445

## FIGURE 5

CCTGACAGAAGTCCCCGGAGCTGGGGAGATNCAACATTAAGAAGATGCTGAGCTCTGGT  
GCCNTTTGGCTCTAATTCTGCCACACAGAGAACAGTCGGCCTATTGTCAACCTTTGTT  
TCCCGGGACCTGGTGGCAGTTCTGCAGCCACAGAGGCAGTGGCGATTTGACAGCCACATA  
CCCTGTGGGTACATGCCATACGGCTGGTTGACGGAAATCCGTGCTGTATCCTGCTTCG  
ACAAGAATAACCCCAGCAACAAACTGGTGAGCACGAGAACACAGTCACGGCGGCCACATC  
AAGAAGTTCACCTCGTCTGCATGGCTCTGTCACTCACGCTCTGTTCGTATGTTGGAC  
ACCCAACGTGTCTGNGAAAATCTTGATAGACATCATCGGAGTGGACTTGCCTTGAGAAC  
TCTGTGTTGTTCTTGCAGATCTTCTCCTTCTCCCAGTTCCAGTCACAGTGAGGGCGCAT  
CTCACCGGGTGGCTGATGACACTGAAGAAAACCTTCGTC

## FIGURE 6

TGACGGAATCCCGGGCTGGGTATCCTGGTTNGACAAGATAAACCCCCAGCAANAAATTGGG  
GAGCAGGGCAAAACAGTNACGGGCAGCCCACATCAAGAAGTTCACCTNGTTGNATGGNTC  
TGTCAACTCACGCTNTGTTCGTATGTTGGACACCCAAAGTGGAGAAAATTGGAT  
AGACATNATCGGAGTGGANTTGCCTTGAGAANTTGNNGNTGTTCCCTTGCGGATTTCT  
CCTTTCCCAGTTCCAGTCACAGNGAGGGCGCATCTCACCGGGNGGNTGATGACANTGAAG  
AAAACCTTGTCCCTGCCCTCAGCTNTTGGTGCAGTCATTGTCCTNATNGCCAGCCTGTTG  
GGTCCTACCCTACCTGGGGTGCACGGTGCACCGCTGGCGTGGTTCCCTCCTGGCGGGCA

## **FIGURE 7**

TATTCCCAGTTCCGGTCACGGGGAGGGCGATNTCACCGGGTGGCTGANGACACTGAAGAAA  
ACCTTNGTCCTTGCCCCCAGNTTGTGNTGCGGATNATCGTCCTCATGCCAGCCTNGTGGT  
CCTACCCTACCTGGGGGTGCACGGTGAGAC

## FIGURE 8

GCCCCGCGCCCGGCGCCGGCGCCCAGGCCGGGAGCCACCGCCATGGGGCCTGCCTGGGA  
GCCTGCTCCCTGCTCAGCTGCGCGTCCTGCCTCTGCGGCTCTGCCCTGCATCCTGTGCAG  
CTGCTGCCCGCCAGCCAACTCCACCGTGAGCCGCCTCATCTTACGTTCTTCTTCTTCC  
TGGGGGTGCTGGTGTCCATCATTATGCTGAGCCCGGGCGTGGAGAGTCAGCTCTACAAGCTG  
CCCTGGGTGTGTGAGGAGGGGCCGGATCCCCACCGTCTGCAGGGCACATCGACTGTGG  
CTCCCTGCTTGGCTACCGCGCTGTCTACCGCATGTGCTTGCACGGCGGCCCTCTTCTTCT  
TCTTTTCACCCCTGCTCATGCTCTGCGTGAGCAGCAGCCGGACCCCCGGCTGCCATCCAG  
AATGGGTTTGGTTCTTAAGTTCTGATCCTGGTGGGCCTCACCGTGGTGCCTTCTACAT  
CCCTGACGGCTCCTCACCAACATCTGGTTCTACTTCGGCGTGTGGCTCCTCCTTCA  
TCCTCATCCAGCTGGTGTGCTCATCGACTTGCACACTCCTGGAACACCAGCGGTGGCTGGC  
AAGGCCGAGGAGTGCATTCCCGTGCCTGGTACGCAGGCCTTTCTTCACTCTCCTTCTT  
CTACTTGCTGTGATCGCGGCCGTGGCGCTGATGTTCATGTACTACACTGAGCCCAGCGGCT  
GCCACGAGGGCAAGGTCTTCATCAGCCTCAACCTCACCTCTGTGTCTGCGTGTCCATCGCT  
GCTGTCCTGCCAAGGTCCAGGACGCCAGCCAACCTGGGTCTGCTGCAGGCCTCGGTCT  
CACCCCTACACCATGTTGTCACCTGGTCAGCCCTATCCAGTATCCCTGAACAGAAATGCA  
ACCCCCATTGCCAACCCAGCTGGCAACGAGACAGTTGTGGCAGGCCCGAGGGCTATGAG  
ACCCAGTGGTGGATGCCCGAGCATTGTGGCCTCATCATCTTCCCTGTGCACCCCTTT  
CATCAGTCTGCGCTCCTCAGACCACCGCAGGTGAACAGCCTGATGCAGACCGAGGAGTGCC  
CACCTATGCTAGACGCCACACAGCAGCAGCAGCAGCAGGTGGCAGCCTGTGAGGGCCGGGCC  
TTTGACAACGAGCAGGACGGACGGCGTCACCTACAGCTACTCCTTCCACTTCTGCCTGGTGCT  
GGCCTCACTGCACGTCTGATGACGCTCACCAACTGGTACAAGCCGGTGAGACCCGGAAGA  
TGATCAGCACGTGGACCGCCGTGGGTGAAGATCTGTGCCAGCTGGCAGGGCTGCTCCTC  
TACCTGTGGACCCCTGGTAGCCCCACTCCTCTGCGCAACCGCGACTTCAGTGAGGCAGCCT  
CACAGCCTGCCATCTGGTGCTCCTGCCACCTGGTGCCTCTGGCTCGGTGACAGCCAACCT  
GCCCTCCCCACACCAATGCCAGGCTGAGCCCCCACCCCTGCCAGCTCCAGGACCTG  
CCCCCTGAGCCGGGCCCTCTAGTCGTAGTGCCTCAGGGTCCGAGGAGCATCAGGCTCCTGCA  
GAGCCCCATCCCCCGCCACACCCACACGGTGGAGCTGCCCTTCCCTCCCTCCCTGT  
TGCCCTACTCAGCATCTGGATGAAAGGGCTCCCTGTGCTCAGGCTCCACGGGAGCGGG  
CTGCTGGAGAGAGCGGGGAACCTCCACACAGTGGGCATCCGGCACTGAAGCCCTGGTGT  
CCTGGTCACGTCCCCCAGGGGACCCCTGCCCTGGACTTCGTGCCTTACTGAGTCTCT  
AAGACTTTCTAATAAACAGCCAGTGCCTGTAAAAAAA

## **FIGURE 9**

MGACLGACSLSCASCLCGSAPCILCSCCPASRNSTVSRLIFTFFLFLGVLVSIIMLSPGVE  
SQLYKLPWVCEEGAGIPTVLQGHIDCGSLLGYRAVYRMCFATAAFFFFFTLLMLCVSSRD  
PRAAIQNGFWFFKFLILVGLTVGAFYIPDGSFTNIWFYFGVVGSLFILIQLVLLIDFAHSW  
NQRWLGAEECDRSAWYAGLFFFLLFYLLSIAAVALMFMYYTEPSGCHEGKVFISLNLTFC  
VCVSIAAVLPKVQDAQPNSGILLQASVITLYTMFVTWSALSSIPEQKCNPHLPTQLGNETVVA  
GPEGYETQWWDAPSIVGLIIFLLCTLFISLRSSDHRQVNSLMQTEECPPMLDATQQQQQQVA  
ACEGRAFDNEQDGVTYSYSFFHFCLVLASLHVMMTLTNWYKPGETRKMISTWTAVWVKICAS  
WAGLLLWTLVAPLLLNRDFS

**Signal sequence:**

amino acids 1-20

**Transmembrane domains:**

amino acids 40-58, 101-116, 134-150, 162-178, 206-223, 240-257,  
272-283, 324-340, 391-406, 428-444

## FIGURE 10

GAGCGAGGCCGGGACTGAAGGTGTGGTGTGAGCCCTCTGGCAGAGGGTTAACCTGGTC  
AAATGCACGGATTCTCACCTCGTACAGTTACGCTCTCCCGCGCACGTCCGAGGACTTGA  
AGTCCTGAGCGCTCAAGTTGTCCGTAGGTCAGAGAAGGCCATGGAGGTGCCACCGGC  
ACCGCGGAGCTTCTCTGTAGAGCATTGTGCCTATTCCCCGAGTCTTGCTGCCAAGCTG  
TGACTGCCGATTCGGAAGTCCTTGAGGAGCGTCAGAACGGCTTCCCTACGTCCCAGAGCCC  
TATTACCGGAATCTGGATGGACCGCCTCCGGAGCTGTTGGCAAAGATGAACAGCAGAG  
AATTCAAAGGACCTTGCTAATATCTGTAAGACGGCAGCTACAGCAGGCATCATTGGCTGGG  
TGTATGGGGAATACCAGCTTTATTCATGCTAAACAACAATACATTGAGCAGAGCCAGGCA  
GAAATTATCATAACCGGTTGATGCTGTGCAATCTGCACATCGTGTGCCACACGAGGCTT  
CATTGTTATGGCTGGCGCTGGGTTGGAGAACTGCAGTGTGACTATATTCAACACAG  
TGAAACACTAGTCTGAATGTATACCGAAATAAGATGCCTTAAGCCATTGTAATTGCAGGA  
GCTGTCACGGGAAGTCTTTAGGATAAACGTAGGCCTGCGTGGCTGGTGGCTGGCAT  
AATTGGAGCCTGCTGGCACTCCTGTAGGAGGCCTGCTGATGGCATTCAAGTACGCTG  
GTGAGACTGTTAGGAAAGAAAACAGAAGGATCGAAAGGCACTCCATGAGCTAAACTGGAA  
GAGTGGAAAGGCAGACTACAAGTTACTGAGCACCTCCCTGAGAAAATTGAAAGTAGTTACG  
GGAAGATGAACCTGAGAATGATGCTAAGAAAATTGAAGCACTGCTAAACCTCCTAGAAACC  
CTTCAGTAATAGATAAACACAAGACAAGGACTGAAAGTGCTCTGAACCTCACTGGAGA  
GCTGAAGGGAGCTGCCATGTCCGATGAATGCCAACAGACAGGCCACTTTGGTCAGCCTGC  
TGACAAATTAAAGTGTGGTACCTGTGGTGGCAGTGGCTTGCTTTGTCTTTCTTTCTT  
TTTAACTAAGAATGGGCTGTTGTACTCTCACTTACTTATCCTAAATTAAATACATACT  
TATGTTGTATTAATCTAATATGCATACATGGATATATCCACCCACCTAGATTTAA  
GCAGTAAATAAACATTGCAAAAGATTAAAGTTGAATTACAGTT

## FIGURE 11

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA23318
><subunit 1 of 1, 285 aa, 1 stop
><MW: 32190, pI: 9.03, NX(S/T): 2
MEVPPPAPRSFLCRALCLFPRVFAAEAVTADSEVLEERQKRLPYVPEPYYPESGWDRRLRELF
GKDEQQRISKDLANICKTAATAGIIGWVYGGIPAFIHAKQQYIEQSQAEIFYHNRFDQSAH
RAATRGFIRYGWRWGRTAVFVTIFNTVNTSLNVYRNKDALSHFVIAGAVTGSLFRINVGLR
GLVAGGIIGALLGTPVGGLLMAFQKYAGETVQERKQKDRKALHELKLEEWKGRLQVTEHLPE
KIESSLREDEPENDAKKIEALLNLPRNPSVIDKQDKD
```

**Important Features:**

**Signal Peptide:**

amino acids 1-24

**Transmembrane domains:**

amino acids 76-96 and 171-195

**N-glycosylation site:**

amino acids 153-156

## **FIGURE 12**

CGGAAGTCCCTTGAGGAGCGTCAGAAGCGGCTTCCCTACGTCCCAGAGCCCTATTACCCGGA  
ATCTGGATGGGACCGCTCCGGGAGCTGTTGGCAAAGATGAACAGCAGAGAATTCAAAGGA  
CCTTGCTAATATCTGTAAGACGGCAGCTACAGCAGGCATCATTGGCTGGGTATGGGGAA  
TACCAGCTTTATTCATGCTAAACAACAATACATTGAGCAGAGCCAGGCAGAAATTATCAT  
AACCGGTTTGTGCTGTGCAATCTGCACATCGTGCTGCCACACGAGGCTTCATTGTTCATG  
GCTGGCGCCGAACC

## **FIGURE 13**

TCAAGTTGTCCGTAGGTCGAGAGAAGGCCATGGAGGTGCCGCCACCGGACCGCGGAGCTT  
TTTCTGTAGAGCATTGTGCCTATTCGGAGTTTGCTGCCGAAGCTGTGACTGCCGAT  
TCGGAAGTCCTTGAGGAGCGTCAGAACGGCTCCCTACGTCCCAGAGCCCTATTACCCGGA  
ATTTGGATGGGACCGCCTCCGGAGCTGTTGGCAAAGATGAACAGCAGAGAAATTCAAAGG  
ACCTTGCTGATATNTGTAAGACGGCAGCTACAGCAGGCATCATTGGCTGGGTGTATGGGGGA  
ATACCAGCTTTATTGNTAAACAACAATACATTGAGCAGAGCCAGGCAGAAATTATNA  
TAACC

## **FIGURE 14**

GAGCCGCCGCCGCGCGCGCGCAGCCCCAGGCCGGCCCCACCGTCT  
GCGTTGCTGCCCGCCTGGGCAGGCCAAAGGAAGGACAAGCAGCTGTCAAGGAACCT  
CCGCCGGAGTCGAATTACGTGCAGCTGCCGGCAACCACAGGTTCAAGATGGTTGCCGGG  
GCTTCGCGTGTCCAAGAACTGCCTGTGCCCTCAACCTGCTTACACCTGGTAGTCTG  
CTGCTAATTGGAATTGCTGCGTGGGCATTGGCTTGGCTGATTCCAGTCTCCGAGTGGT  
CGCGTGGTCATTGCAGTGGCATCTTCTTGCTTGTGCTTACTGGGTCTGATTGGAG  
CTGTAAAACATCATCAGGTGTTGCTATTTTTATATGATTATTCTGTTACTGTATTTATT  
GTTCAGTTCTGTATCTGCGCTTGTAGCCCTGAACCAGGAGCAACAGGGTCAGCTTCT  
GGAGGTTGGTTGAAACAATACGGCAAGTGCTCGAAATGACATCCAGAGAAATCTAAACTGCT  
GTGGGTTCCGAAGTGTAAACCAAATGACACCTGTCTGGCTAGCTGTGTTAAAGTGACCAC  
TCGTGCTGCCATGTGCTCCAATCATAGGAGAATATGCTGGAGAGGTTTGAGATTGTTGG  
TGGCATTGGCCTGTTCTCAGTTTACAGAGATCCTGGGTGTTGGCTGACCTACAGATA  
GGAACCAGAAAGACCCCGCGCGAACCTAGTGCATTCTTGATGAGAAAACAAGGAAGAT  
TTCCTTCGTATTATGATCTGTTCACTTCTGTAATTTCTGTTAAGCTCCATTGCCAGT  
TTAAGGAAGGAAACACTATCTGGAAAAGTACCTTATTGATAGTGGATTATATATTTACT  
CTATGTTCTCTACATGTTTTCTTCCGTTGCTGAAAATATTGAAACTTGTGGTCTC  
TGAAGCTCGGTGGCACCTGGAATTACTGTATTCAATTGCTGGGACTGTCCACTGTGGCCTT  
TCTTAGCATTTCACCTGCAGAAAAACTTGTATGGTACCACTGTGTTGGTATATGGTGA  
TCTGAACGTACATCTCACTGGTATAATTATATGTAGCACTGTGCTGTAGATAGTCCCTAC  
TGGAAAAAGAGTGGAAATTATTAAACAGAAAGTATGAGATCCTGTTATGTTAAGGGAAA  
TCCAAATTCCAATTGGTCTTTAGGAAAGATTGTTGGTAAAAAGTGTAGTA  
AAAAATGATAATTACTGTAGTCTTTATGATTACACCAATGTATTCTAGAAATAGTTAT  
GTCTTAGGAAATTGTGGTTAATTGACTTTACAGGTAAGTGCAAAGGAGAAGTGGTT  
CATGAAATGTTCAATGTATAATAACATTACCTCAGCCTCCATCAGAAATGGAACGAGTTT  
TGAGTAATCAGGAAGTATATCTATATGATCTGATATTGTTATAATAATTGAAGTCTAA  
AAGACTGCATTAAACAGTTAGTATTAAATGCGTGGCCCACGTAGCAAAAGATATTG  
ATTATCTTAAAATTGTTAAATACCGTTTATGAAATTCTCAGTATTGTAACAGCAACTT  
GTCAAACCTAAGCATATTGAATATGATCTCCATAATTGAAATTGAAATCGTATTGTG  
GCTCTGTATATTCTGTTAAAAATTAAAGGACAGAAACCTTCTTGTATGCATGTTGA  
ATTAAAAGAAAGTAATGGAAG

## **FIGURE 15**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA39979
><subunit 1 of 1, 204 aa, 1 stop
><MW: 22147, pI: 8.37, NX(S/T): 3
MVCGGFACSKNCLCALNLLYTLVSLLLIGIAAWGIGFGLISSLRVVGVVIAVGIFLFLIALV
GLIGAVKHHQVLLFFYMIILLLVFIVQFSVSCACLAQNQQGQQLLEVGVNNNTASARNDIQR
NLNCCGFRSVNPNDTCLASCVKSDHSCSPCAPIIGEYAGEVLRFVGGIGLFFSFTIELGVWL
TYRYRNQKDPRANPSAFL
```

**Signal Peptide:**

amino acids 1-34

**Transmembrane domains:**

amino acids 47-63, 72-95 and 162-182

## **FIGURE 16**

TGATTGGAGCTGTAAAAANTCTTCAGGTGTTGTNATTTTTATATGATTATTCTGTAANT  
TGTATTTATTGTTCAGTTNTGTATCTTCAGCTTGTTAGCCNTGAACCAGGAGAACAGG  
GTCAGNTNTGGAGGTTGGTTGGAACAATACGGCAAGTGCTCGAAATGACATCCAGAGAAAT  
NTAAACTGCTGTGGGTTCCGAAGTGTAAACCAAATGACACCTGTNTGGCTAGCTGTGTTAA  
AAGTGACCACTNGTGCTGCCATGTGCTCCAATCATAGGAGAATATGCTGGAGAGGTTTGAC  
GATTGTTGGTGGCATTGGCCTGTTNTCAGTTTACAGAGATCCTGGGTGTTGGCTGACC  
TACAGATAACAGGAACCAAG

## **FIGURE 17**

AATCCCAAATTCCCCAATTTTTGGNCTTTAGGGAAAGATGTGTTGGTAAAAAGTGT  
TAGTATAAAAATGATAATTACTTGTAGTCCTTATGATTACACCAATGTATTCTAGAATAG  
TTATGTCTTAGGAAATTGTGGTTAACCTTGACTTTACAGGTAAGTGCAAAGGAGAAGTG  
GTTTCATGAAATGTTCTAATGTATAAACATTACCTCAGCCTCCCATCAGAATGGAACG  
AGTTTGAGTAATCCAGGAAGTATATCTATATGATCTTGATATTGTTTATATAATTGAAAG  
TCTAAAAGACTGCATTTAAACAAGTTAGTATTAATCGTTGCCACGTAGCAAAAGAT  
ATTGATTATCTTAAAATTGTTAAATACCGTTCATGAAAGTTCTCAGTATTGTAACAGC  
AACTTGTCAAACCTAAGCATATTGAATATGATCTCCATAATTGAAATTGAAATCGTATT  
GTGTGGAGGAAATGGCAATCTTATGTGTGCTGAAGGACACAGTAAGAGCACCAAGTTGTGCC  
CCACTTGC

## **FIGURE 18**

ATGATTATTCTGTTACTTGTATTTATTGTTCAGTTTATGGTATCTTCGCGCTTGTTAGCCC  
CTGAAACCAGGAGCAACAGGGNNNCAGCTTCCCTGGAGGTTGGCAACAATCACGGCCAAG  
TGACTCCGCAAATGACATCCCAGAGAAATCCTAAACTGCTGTGGGTTCCGAAGTGTAAACCC  
AAATGACACCTGTCTGGCTNGCTGTGTTAAAAGTGACCACTCGTGCTGCCATGTGCTCCAA  
TCATAGGAGAATATGC

## **FIGURE 19**

CAGTCACCATGAAGCTGGCTGTCTCATGGCCTGGCCCTCACCTTCCCTGGTGTG  
CTCTGGTGGCCAGATGCTACTGGCTGCCAGTTGAGACGCTGCAGTGTGAGGGACCTGT  
CTGCACTGAGGAGAGCAGCTGCCACACGGAGGATGACTGACTGATGCAAGGAAGCTGGCT  
TCCAGGTCAAGGCCTACACTTCAGTAACCCCTCCACCTGATTGTGCTATGACTGGCTG  
ATCCTCCAAGGTCCAGCCAAGCCAGTTTGAGGGGACCTGCTGGTTCTGCCTGCCAGGC  
CTGGCAAGACTGGCCACTGACTCAGGTGACCTCTACCGAGATGGCTCAGCTCTGGTCCCC  
CCGGGCCTAACAGGAATTCTCATCACCGTGGTACAAAAGGCAGACAGGGCACTACCAC  
TGCAGTGGCATCTTCAGAGCCCTGGCTGGATCCCAGAAACAGCATCTGTTGGCTAT  
CACAGTCCAAGAACTGTTCCAGCGCAATTCTCAGAGCTGTACCCCTCAGCTGAACCCAAG  
CAGGAAGCCCCATGACCCTGAGTTGTAGACAAAGTGGCCCTGCAGAGGTAGCTGCCGC  
CTCCTCTCTCTACAAGGATGGAAGGATAGTCAAAGCAGGGGCTCTCCTCAGAATT  
CCAGATCCCCACAGCTTCAGAAGATCACTCCGGTCATACTGGTGTGAGGCAGCCACTGAGG  
ACAACCAAGTTGGAAACAGAGCCCCAGCTAGAGATCAGAGTGCAGGGTGTCCAGCTCT  
GCTGCACCTCCCACATTGAATCCAGCTCTCAGAAATCAGCTGCCAGGAACGTCTGA  
GGAGGCCCTGGGCCTCTGCCTCCGCCAACCCATCTCTGAGGATCCAGGCTTTCTT  
CTCCTCTGGGATGCCAGATCCTCATCTGTATCACCAGATGGCCTTCTCTCAAACACATG  
CAGGATGTGAGAGTCTCCTCGGTACCTGCTCATGGAGTTGAGGAATTATCTGCCACCA  
GAAGCCTGGGACCACAAAGGCTACTGCTGAATAGAAGTAAACAGTTCATCCATGATCTCACT  
TAACCACCCAATAAATCTGATTCTTATTTCTCTGCACATATGCATAAGTA  
CTTTTACAAGTTGTCCTCAGTGTGTTAGAATAATGTAGTTAGGTGAGTGTAAATAATT  
ATATAAAAGTGAGAATTAGAGTTAGCTATAATTGTGTATTCTCTTAAACACAACAGAATT  
TGCTGTCTAGATCAGGAATTCTATCTGTATATCGACAGAATGTTGTGATTAAAGAGAA  
CTAATGGAAGTGGATTGAATAACAGCAGTCTCAACTGGGGCAATTGGCCCCCAGAGGACA  
TTGGCAATGTTGGAGACATTGGTCATTATAACTTGGGGGTGGGGATGGTGGATGT  
GTGTCTACTGGCATCCAGTAAATAGAAGCCAGGGGTGCCGCTAACACATCCTATAATGCACAG  
GGCAGTACCCCACAACGAAAAATACTGGCCAAAATGTCAGTGTACTGAGTTGAGAAA  
CCCCAGCCTAATGAAACCCCTAGGTGTTGGCCTGGGAATGGGACTTGTCCCTCTAATT  
TATCTCTTCCAGCCTATTCTAGCTATTCTACTGACATACCACTCTTAGCTGGTGTATG  
GTCTGTTCTTAGTTCTAGTTGATCCCTCAAAAGCATTATGTTGAAATCTTAATCCCC  
AAGGTGATGGCATTAAAGAAGTGGCCTTGGGAAGTGATTAGATCAGGAGTGCAGGCCCTC  
ATGATTAGGATTAGTGCCTTATTAAAAAGGCCAGAGAGCTAACTCACCTCCACCAT  
ATGAGGACGTGGCAAGAAGATGACATGTATGAGAACAAAAACAGCTGTCGCCAACACCG  
ACTCTGTCGTTGCCTTGATCTGAACCTCCAGCCTCAGAACTATGAGAAATAAAATTCTGG  
TTGTTGTAGCCTAA

## FIGURE 20

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA40594
><subunit 1 of 1, 359 aa, 1 stop
><MW: 38899, pI: 5.21, NX(S/T): 0
MKLGCVLMMAWALYLSLGVLWVAQMLLAASFETLQCEGPVCTEESSCHTEDDLTDAREAGFQV
KAYTFSEPFHLIVSYDWLILQGPAKPVFEGDLLVLRCQAWQDWPLTQVTFYRDGSALGPPGP
NREFSITVVQKADSGHYHCSGIFQSPGPGIPETASVVAITVQELFPAPILRAVPSAEPQAGS
PMTLSCQTKLPLQRSAARLLFSFYKDGRIVQSRGLSSEFQIPTASEDHSGSYWCEAATEDNQ
VWKQSPQLEIRVQGASSSAAPTLNPAPQKSAAPGTAAPEEAPGPLPPPPTPSSEDPGFSSPL
GMPDPHLYHQMGLLLKHMQDVRVLLGHLLMELRELSGHQKPGTTKATAE
```

**Signal sequence:**

amino acids 1-17

**Leucine zipper pattern sequence:**

amino acids 12-33

**Protein kinase C phosphorylation site:**

amino acids 353-355

## **FIGURE 21**

CCACACGCGTCCGCCAACCGCGTCCGCCAACGGGTCCGCCACCGCTCCGGGCCACAGAAAGTT  
TGAGCCTTTGGTAGCAGGAGGCTGGAAGAAAGGACAGAAGTAGCTCTGGCTGTGATGGGG  
ATCTTAACGGGCCTGCTACTCCTGGGCACCTAACAGTGGACACTTATGGCCGTCCCACCT  
GGAAGTGCAGAGAGTGTAAACAGGACCTGGAAAGGGATGTGAATCTTCCTGCACCTATG  
ACCCCTGCAAGGCTACACCCAAGTCTTGGTGAAGTGGCTGGTACAACGTGGCTCAGACCC  
GTCACCACATCTTCTACGTGACTCTTCTGGAGACCATATCCAGCAGGCAAAGTACCAAGGGCG  
CCTGCATGTGAGCCACAAGGTTCCAGGAGATGTATCCCTCAATTGAGCACCCCTGGAGATGG  
ATGACCGGAGCCACTACACGTGTAAGTCACCTGGCAGACTCCTGATGGCAACCAAGTCGTG  
AGAGATAAGATTACTGAGCTCCGTGTCAGAAACTCTCTGTCTCCAAGCCCACAGTGACAAC  
TGGCAGCGGTTATGGCTTACGGTGCCTCAGGGAATGAGGATTAGCCTCAATGCCAGGCTC  
GGGGTTCTCCTCCATCAGTTATTTGGTATAAGCAACAGACTAATAACCAGGAACCCATC  
AAAGTAGCAACCCCTAACGTACCTTACTCTCAAGCCTGCCGTGATAGCCGACTCAGGCTCCTA  
TTTCTGCACTGCCAACGGCCAGGTTGGCTCTGAGCAGCACAGCATTGTGAAGTTGTGG  
TCAAAGACTCCTCAAAGCTACTCAAGACCAAGACTGAGGCACCTACAACCATGACATACCCC  
TTGAAAGCAACATCTACAGTGAAGCAGTCCTGGGACTGGACCACTGACATGGATGGCTACCT  
TGGAGAGACCAGTGCTGGGCCAGGAAAGAGCCTGCCTGTCTTGCCTCATCCTCATCATCT  
CCTTGTGCTGTATGGGTTTTACCATGGCTATATCATGCTCTGTCGGAAGACATCCCAA  
CAAGAGCATGTCTACGAAGCAGCCAGGTAAGAAAGTCTCTCCTTCCATTGGACCCGT  
CCCTGCCCTCAATTGATTACTGGCAGGAATGTGGAGGAAGGGGGTGTGGCACAGACCC  
AATCCTAACGGCCGGAGGCCTCAGGGTCAGGACATAGCTGCCTCCCTCTCAGGCACCTT  
CTGAGGTTGTTTGGCCCTCTGAACACAAAGGATAATTAGATCCATCTGCCCTCTGCTTCC  
AGAATCCCTGGGTGGTAGGATCCTGATAATTAAATTGGCAAGAATTGAGGCAGAAGGGTGGGA  
AACCAAGGACCACAGCCCCAAGTCCCTCTTATGGGTGGTGGCTCTGGGCCATAGGGCACA  
TGCCAGAGAGGCCAACGACTCTGGAGAAACCATGAGGGTGGCCATCTCGCAAGTGGCTGCT  
CCAGTGATGAGCCAACCTCCAGAATCTGGCAACAAACTACTCTGATGAGCCCTGCATAGGA  
CAGGAGTACCAAGATCATGCCAGATCAATGGCAACTACGCCGCCCTGCTGGACACAGTTCC  
TCTGGATTATGAGTTCTGGCACTGAGGGCAAAGTGTCTGTTAAAATGCCCATAGGC  
CAGGATCTGCTGACATAATTGCCCTAGTCAGTCCTGCCCTCTGCATGGCCTTCTCCCTGCT  
ACCTCTTCCCTGGATAGCCCAAAGTGTCCGCCCTACCAACACTGGAGCCGTGGAGTCCT  
GGCTTGCCTGGATTGCAAGATGCACTCAAGTAAGCCAGCTGCTGGATTGGCTCTGG  
GCCCTCTAGTATCTGCCGGGGCTTCTGGTACTCCCTCTAAATACCAAGAGGGAAAGATG  
CCCCTAGCACTAGGACTGGTCATCATGCCCTACAGACACTATTCAACTTGGCATCTGCCA  
CCAGAAGACCCGAGGGAGGCTCAGCTGCCAGCTCAGAGGACCAGCTATATCCAGGATCAT  
TTCTCTTCTTCAGGGCCAGACAGCTTTAATTGAAATTGTTATTTCACAGGCCAGGGTTCA  
GTTCTGCTCCTCCACTATAAGTCTAATGTTCTGACTCTCCTGGTGTCAATAATATCTA  
ATCATAACAGC

## **FIGURE 22**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45416
><subunit 1 of 1, 321 aa, 1 stop
><MW: 35544, pI: 8.51, NX(S/T): 0
MGILLGLLLGHLTVDTYGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLVKWLVQRGS
DPVTIFLRDSSGDHIQQAKYQGRLHVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQTPDGNQ
VVRDKITELRVQKLSVSKPTVTGSGYGFTVPQGMRISLQCQARGSPPISYIWYKQQTNQE
PIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSEQHSDIVKFVVKDSSKLLKTTEAPTTMT
YPLKATSTVKQSWDWTMDGYLGETSAGPGKSLPVFAIIILIIISLCCMVFPMAYIMLCRKT
SQQEHVYEAR
```

**Signal Sequence:**

amino acids 1-19

**Glycosaminoglycan attachment site:**

amino acids 149-152

**Transmembrane domain:**

amino acids 282-300

## **FIGURE 23**

GGCCGGGAGCCCCTGCCAGGGCACGGGGCGGGCGGGCTCCGCCGGCACAT  
GGCTGCAGCCACCTCGCGCACCAGGGCGCCAGCTGCCAGGTCCGTCGGA  
GGCGCCGGCGCCGGAGCCAAGCAGCAACTGAGCGGGAAAGCGCCCGTCCGGGATC  
**GGGATG**TCCCTCCTCTCTCTTGCTAGTTCTACTATGTTGAACTTGGGACTCA  
CACTGAGATCAAGAGAGTGGCAGAGGAAAAGGTCACTTGCCCTGCCACCATCAACTGGGGC  
TTCAGAAAAAGACACTCTGGATATTGAATGGCTGCTACCGATAATGAAGGGAACCAAAA  
GTGGTGTACTACTCCAGTCGTATGTCTACAATAACTGACTGAGGAACAGAACGGCCG  
AGTGGCCTTGCTTCAATTCTGGCAGGAGATGCCTTGCAAGATTGAACCTCTGAAGC  
CCAGTGATGAGGGCCGGTACACCTGTAAGGTTAAGAATTCAAGGGCCTACGTGTGGAGCCAT  
GTCATCTTAAAGTCTTAGTGAGACCATCCAAGCCAAAGTGTGAGTTGGAAGGAGAGCTGAC  
AGAAGGAAGTGACCTGACTTGCACTGTGAGTCATCCTCTGGCACAGAGCCCATTGTGTATT  
ACTGGCAGCGAATCCGAGAGAAAAGAGGGAGAGGATGAACGTCTGCCTCCAAATCTAGGATT  
GACTACAACCACCCCTGGACGAGTTCTGCTGAGAATCTTACCATGTCTACTCTGGACTGTA  
CCAGTGACAGCAGGCAACGAAGCTGGAGGAAAGCTGTGTGGCGAGTAAGTACAGT  
ATGTACAAAGCATCGGCATGGTGCAGGAGCAGTGACAGGCATAGTGGCTGGAGCCCTGCTG  
ATTTCTCTTGGTGTGGCTGCTAATCGAAGGAAAGACAAAGAAAGATATGAGGAAGAAGA  
GAGACCTAATGAAATTGAGAAGATGCTGAAGCTCCAAAAGCCGTCTTGTGAAACCCAGCT  
CCTCTCCTCAGGCTCTGGAGCTCACGCTCTGGTTCTCCTCCACTCGCTCCACAGCAAAT  
AGTGCCTCACGCAGCCAGCGACACTGTCAACTGACGCAGCACCCAGCCAGGGCTGGCAC  
CCAGGCATAACGCCTAGTGGGCCAGAGGTGAGAGGTTCTGAACCAAAGAAAGTCCACCATG  
CTAATCTGACCAAAGCAGAAACCACACCCAGCATGATCCCCAGCCAGAGCAGAGCCTTCAA  
ACGGCT**TGA**ATTACAATGGACTTGACTCCCACGCTTCTAGGAGTCAGGGTCTTGGACTC  
TTCTCGTCATTGGAGCTCAAGTCACCAGCCACACAACCAGATGAGAGGTCATCTAAGTAGCA  
GTGAGCATTGCACGGAACAGATTAGCATTGAGCATTCTTCTTACAATACCAAAGCAA  
AGGATGTAAGCTGATTGATCTGTAAAAGGCATCTTATTGTGCCCTTAGACCAGAGTAAGGG  
AAAGCAGGAGTCCAAATCTATTGTTGACCAGGACCTGTGGTGAGAAGGTTGGGAAAGGTG  
AGGTGAATATACTAAAACCTTTAATGTGGATATTGTATCAGTGCTTGATTACAATT  
TTCAAGAGGAATGGATGCTGTTGTAATTCTATGCAACTTCTGCAAACATTATTGGATT  
ATTAGTTATTCAAGACAGTCAGCAGAACCCACAGCCTTATTACACCTGTCTACACCATGTAC  
TGAGCTAACCACTCTAAGAAACTCCAAAAAGGAAACATGTGTCTTCTATTCTGACTTAAC  
TTCATTGTCATAAGGTTGGATATTAAATTCAAGGGAGTTGAAATAGTGGAGATGGAGA  
AGAGTGAATGAGTTCTCCACTCTACTAACTCACTATTGTATTGAGCCAAAATAAC  
TATGAAAGGAGACAAAATTGTGACAAAGGATTGTGAAGAGCTTCCATCTCATGATGTT  
ATGAGGATTGTTGACAAACATTAGAAATATATAATGGAGCAATTGTGGATTCCCTCAAAT  
CAGATGCCCTCAAGGACTTCCCTGCTAGATATTCTGGAAGGAGAAAATACAACATGTCTT  
TATCAACGTCCCTAGAAAGAATTCTCTAGAGAAAAGGGATCTAGGAATGCTGAAAGATTA  
CCCAACATACCATTATAGTCCTCTTCTGAGAAAATGTGAAACCAAGGAAATTGCAAGACTGG  
GTGGACTAGAAAGGGAGATTAGATCAGTTCTTCTTAATATGTCAAGGAAGGTAGCCGGCA  
TGGTGCCAGGCACCTGTAGGAAAATCCAGCAGGTGGAGGTTGCAGTGAGCCGAGATTATGCC  
ATTGCACTCCAGCCTGGGTGACAGAGCGGGACTCCGTCTC

## **FIGURE 24**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45419
><subunit 1 of 1, 373 aa, 1 stop
><MW: 41281, pI: 8.33, NX(S/T): 3
MSLLLLLLSYYVGTGLTHTEIKRVAEEKVTLPCHHQLGLPEKDTLDIEWLLTDNEGNQKV
VITYSSRHVYNNLTEEQKGRVAFASNFLAGDASLQIEPLKPSDEGRYTCKVKNSGRYVWSHV
ILKVLVRPSKPCKELEGELTEGSDLTLQCESSSGTEPIVYYWQRIREKEGEDERLPPKSRID
YNHPGRVLLQNLTMYSGLYQCTAGNEAGKESCVVRTVQYVQSIGMVAGAVTGIVAGALLI
FLLVWLILLRKDKERYEEEERPNEIREDAEAPKARLVKPSSSSGSRSSRGSSSTRSTANS
ASRSQRTLSTDAAQPGLATQAYSLVGPEVRGSEPKVHANLTKAETTPSMIPSQSRAFQTV
```

**Signal sequence:**

amino acids 1-16

**Transmembrane domain:**

amino acids 232-251

## FIGURE 25

GTGGTTCCCTTGCTCTCGCGCCCAGTCCTCCTCCCTGGTTCTCTCAGCCGCTGTCGGAGGAGAGCACCCGGA  
GACCGGGGCTGCAGTCGCGCGCTTCTCCCCGCTGGCGGCTCGCCGCTGGCAGGTGCTGAGCGCCCTAG  
AGCCTCCCTGCCGCTCCCTCTGCCCGGCGAGCAGTCACATGGGTGTTGGAGGTAGATGGCTCCCG  
GCCCGGGAGGCGCGGTGGATGCCGCTGGCAGAAGCAGCCGCCATTCCAGCTGCCCGCGGCCGGCG  
CCCTGCGAGTCCCCGGTTCAGCATGGGACTCTCTCCGAGCAGCAGCACCGCCCTCGCCTCTGCAGCCGCATC  
GCCCGCCAGCCACAGCACGATGATGCCGCGCTCCCTCTCTGCTGGATTCTTAGCACCACAGCTCAG  
CCAGAACAGAAGGCTGAATCTCATGGCACATACGCCATGTTGACCGTGCACCGGCCAGGTGCTAACCTGT  
GACAAGTGTCCAGCAGGAACCTATGTCCTGAGCATTGTACCAACACAAGCTGCGCTCTGCAGCAGTTGCCCT  
GTGGGACCTTACCAAGGCATGAGAATGGCATAGAGAAATGCCATGACTGTAGTCAGCCATGCCATGGCCAATG  
ATTGAGAAATTACCTTGTGCTGCCCTGACTGACCGAGAAATGCACTTGCCCACCTGGCATGTTCCAGTCTAACGCT  
ACCTGTGCCCCCCATACGGTGTGCTGTGGGTGGGGTGTGCGGAAGAAAGGGACAGAGACTGAGGATGTGCGG  
TGTAAGCAGTGTGCTGGGTACCTCTCAGATGTGCCTCTAGTGTGATGAAATGCAAAGCATAACAGACTGT  
CTGAGTCAGAACCTGGTGTGATCAAGCCGGGACCAAGGAGACAGAACGACTGTGTCGGCACACTCCGCTTC  
TCCAGCTCACCTCACCTCCCGGACAGCCATTTCCACGCCCTGAGCACATGGAAACCCATGAAGTCCCT  
TCCCTCCACTTATGTCCTGAACTCAACAGAACGACTTCTCTGCTCTGTTAGACCAAGGTACTG  
AGTAGCATCCAGGAAGGGACAGTCCCTGACAAACACAAGCTCAGCAAGGGGAGGAAGACGTGAACAAGACCC  
CCAAACCTCAGGTAGTCACCACAGCAAGGCCAACACAGAACATCCTGAGCTGCGCTCATGGAG  
GCCACTGGGGCGAGAAGTCCAGCACGCCATCAAGGCCAACAGGGGACATCCTAGACAGAACCTACACAAG  
CATTGACATCAATGACATTGGCCTGGATGATTGTGCTTTCTGCTGCTGGTCTTGTTGATTGTGGT  
TGCAGTATCGGAAAAGCTGAGGACTCTGAAAAGGGGCCCCGGCAGGATCCAGTGCCTATTGTGGAAAAGGCA  
GGGCTGAAGAAATCCATGACTCCAACCCAGAACCGGGAGAAATGGATCTACTACTGCAATGCCATGGTATCGAT  
ATCCTGAAGCTTGTAGCAGCCAAAGTGGGAGCCAGTGGAAAGATATCTATCAGTTCTTGCAATGCCAGTGAG  
AGGGAGGTTGCTGCTTTCTCAATGGGTACACAGCCGACCAAGGGGCTACGAGCTCTGAGCAGTGAG  
ATCCGGGGCCCCGAGGCCAGCCTGCCAGCTAAATTAGGCCCTGCCAGCACCGGAGAAACGATGTTGAG  
AAGATTGCTGGCTGATGGAAGACACCACCCAGCTGAAACTGACAAACTAGCTCTCCGATGAGCCCCAGCC  
CTTAGCCGAGCCCCATCCCCAGCCCCAACCGGAAACTTGAGAATTCCGCTCTCTGACGGTGGAGGCCCTCCCC  
CAGGACAAGAACAAAGGGCTCTCGTGGATGAGTCGGAGCCCCCTCTCGCTGTGACTCTACATCCAGCGGCTCC  
TCCGCGCTGAGCAGGAACGGTTCTTATTACCAAGAAAAGGACACAGTGTGCGGAGGTACGCCCTGGAC  
CCCTGTGACTTGCAGCCTATCTTGATGACATGCTCCACTTCTAAATCCTGAGGAGCTGCCGTGATTGAAGAG  
ATTCCCCAGGCTGAGGACAAACTAGACCGGCTATTGAAATTATTGGAGTCAAGAGCCAGGAAGCCAGCAGACC  
CTCCCTGGACTCTGTTATGCCATCTCCGACCTGCTGTAAGAACATAGGGACTTGCAATTGAAATTACTCA  
ATTAGTGGCAGGGTGGTTTTAAATTCTCTGTTCTGATTGTTGTTGGGGTGTGTTGTTGTTG  
GTGTTG  
TCCT  
ATACCCACCAAAAGTTTAAAGTCCATATTCTCCATTGGCTTCTATGTTCAAGCTTGCCTGAGGTGTAACTGTTGAA  
TGCACCTAAATTACTTAACCTACCAAAATGCACTGTAACCTTCCACACACTGGATTGTGAGGCTCTAAC  
TTCTTAAAGTATAATGCCATCTGTAACCTTAAAGCAGTCTTATGCTCTTAAACATTACACCTACTTTT  
AAAAACAAATTATTACTATTATTATTGTTGTCCTTATAAATTCTTAAAGGTTAAAGAAAATTAAAGA  
CCCCATTGAGTTACTGTAATGCAATTCAACTTGTAGTTATCTTTAAATATGCTTGTATAGTTCATATTG  
CTGAAACTTGCACACACTATTGCTGATTGTATGGTTTCACTGGACACCGTGTAGAATGCTTGTATTACTG  
TCTTCTTATGCTAATATGCTCTGGCTGGAGAAATGAAATCCTCAAGCCATCAGGATTGCTTGTATTAAAGTGGCTT  
GACAACGGGCCACCAAGAACCTGAACTTCACCTTCTGAGCTGTTGAGACACATTGCTGCACTTT  
GGAAAGTCAAATCAAGTGCAGTGGCGCCCTTCCATAGAGAATTGCCCAGCTTGTAAAAGATGTCTTG  
TTTTTATATACACATAATCAATAGGTCCAATCTGCTCTCAAGGCCCTGGTCTGGTGGGATTCTTCAACCAATT  
ACTTTAATTAAAAATGGCTGCAACTGTAAGAACCCCTGCTGATATATTGCAACTATGCTCCATTACAAATG  
TACCTTCTAATGCTCAGTTGCCAGGTTCCAATGCAAAGGTGGCGTGGACTCCCTTGTGTTGGTGGGGTTGTGG  
GTAGTGGTGAAGGACCGATATCAGAAAAATGCCCTCAAGTGTACTAATTATTAATAAACATTAGGTGTTGTTA  
AAAAAAAAA

## **FIGURE 26**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52594  
><subunit 1 of 1, 655 aa, 1 stop  
><MW: 71845, pI: 8.22, NX(S/T): 8  
MGTPSSSTALASCRIARRATATMIAGSLLLLGFLSTTTAQPEQKASNLIGTYRHVRATG  
QVLTCDKCPAGTYVSEHCTNTSLRVCSSCPVGTFRHENGIEKCHDCSQPCPWPWPMIEKLPCA  
ALTDRECTCPPGMFQSNTCAPHTVCVPVGWRKKGTETEDVRCKQCARGTFSDVPSSVMKC  
KAYTDCLSQNLLVVIKPGTKETDNVCGTLPSFSSSTSPSPGTAIFPRPEHMETHEVPSSTYVP  
KGMNSTESNSSASVRPKVLSSIQEGLVPDNTSSARGKEDVNKTLPNLQVVNHQQGPHHRHIL  
KLLPSMEATGGEKSSTPIKGPKRGHPRQNLHKHFDINEHLPWMIVLFLLLVLVVIVVCSIRK  
SSRTLKKGPRQDPSAIVEKAGLKKSMPTQNREKWIYYCNGHGIDILKLVAAQVGSQWKDIY  
QFLCNASEREVAAFSNGYTADHERAYAALQHWTIRGPEASLAQLISALRQHRRNDVVEKIRG  
LMEDTTQLETDKLALPMSPSPLSPSPPIPSPNAKLENSALLTVEPSPQDKNKGFFVDESEPLL  
RCDSTSSGSSALSRNNGSFITKEKKDTVLRQVRLDPQIFDDMLHFLNPEELRVIEEIPQ  
AEDKLDRLFEIIGVKSQEASQTLDSVYSHLPDLL

**Signal sequence:**

amino acids 1-41

**Transmembrane domain:**

amino acids 350-370

## FIGURE 27

ATGGGAAGCCAGTAACACTGTGGCCTACTATCTCTTCCGTGGGCCATCTACATTGGGA  
CTCGGGATTATGAGGTAGAGGTGGAGGCAGGCCGATGTCAGAGGTCTGAAATAGTCAC  
**CATGGGGAAAATGATCCGCCTGCTGTTGAAGCCCCCTCTCATCCGATCGCTTTGGCC**  
TTGATGATTGAAAATAAGTCCTGTCACCAGATGCACTGCTGTCAGAGATCCTG  
TCACTGCTGCCATTGAAGTTTTCCAATCATCGTCATTGGGATCATTGCATTGATATTAGC  
ACTGGCCATTGGTCTGGCATCCACTCGACTGCTCAGGGAAAGTACAGATGTCGCTCATCCT  
TTAAGTGTATCGAGCTGATAGCTCGATGTGACGGAGTCGGATTGCAAAGACGGGGAGGAC  
GAGTACCGCTGTGTCGGTGGGTGAGAATGCCGTGCTCCAGGTGTTACAGCTGCTTC  
GTGGAAGACCATGTGCTCCGATGACTGGAAGGGTCACTACGCAAATGTTGCCGTGCCAAC  
TGGTTTCCAAGCTATGTGAGTCAGATAACCTCAGAGTGAGCTCGCTGGAGGGCAGTTC  
CGGGAGGAGTTGTGTCATCGATCACCTCTGCCAGATGACAAGGTGACTGCATTACACCA  
CTCAGTATATGTGAGGGAGGGATGTGCTCTGCCACGTGGTACCTTGCACTGCACAGCCT  
GTGGTCATAGAAGGGCTACAGCTACGCATCGTGGGTTGAAACATGTCCTGCTCTCGCAG  
TGGCCCTGGCAGGCCAGCCTCAGTCCAGGGTACCCACCTGTGCCGGGCTCTGTCACTCAC  
GCCCTGTGGATCATCACTGTCACACTGTGTTATGACTGTTACCTCCCCAAGTCATGGA  
CCATCCAGGTGGTCTAGTTCCCTGTTGACAATCCAGCCCCATCCCACGGTGGAGAAG  
ATTGTCTACCACAGCAAGTACAAGCCAAAGAGGCTGGCAATGACATGCCCTATGAAGCT  
GGCCGGGCCACTCACGTTCAATGAAATGATCCAGCCTGTCGCCAAGTCTGAAGAGA  
ACTTCCCCGATGGAAAAGTGTGCTGGACGTCAAGGATGGGGGCCACAGAGGATGGAGGTGAC  
GCCTCCCTGTCCTGAACCACCGCGGCCGTCCTTGTGATTCCAACAAGATGCAACCACAG  
GGACGTGTACGGTGGCATCATCTCCCCCTCCATGCTCTGCCGGCTACCTGACGGGTGGCG  
TGGACAGCTGCCAGGGGACAGCGGGGCCCTGGTGTGTCAGAGAGGAGGCTGTGGAAG  
TTAGTGGGAGCGACCAGCTTGGCATGGCTGCCAGAGGTGAAACAAGCCTGGGTGTACAC  
CCGTGTCACCTCCTGGACTGGATCCACGAGCAGATGGAGAGAGACCTAAAAC**TGAA**  
GAGGAAGGGACAAGTAGCCACCTGAGTTCTGAGGTGATGAAGACAGCCGATCCTCCCT  
GGACTCCCGTGTAGGAACCTGCACACGAGCAGACACCCTGGAGCTTGAGTTCCGGCACCA  
GTAGCTGGGACCACAGGTGCCGCCACACACCAACTAATTGTATTAGAGAC  
AGGGTTTACCATGTTGCCAGGCTGCTCTCAAACCCCTGACCTCAAATGATGTCCTGCTT  
CAGCCTCCACAGTGTGGATTACAGGCATGGGCCACCGCCTAGCCTCACGCTCCTTTC  
TGATCTTCACTAAGAACAAAAGAAGCAGCAACTGCAAGGGCGGCCCTTCCACTGGTCCAT  
CTGGTTTCTCCAGGTCTGCAAATTCTGACGAGATAAGCAGTTATGTGACCTCACG  
TGCAAAGCCACCAACAGCCACTCAGAAAAGACGCCAGAGCAGCCAGAAGTGCAGAACTGCAGTC  
ACTGCACGTTTCATCTCTAGGGACCAACCAACCCCTTCTACTCCTAAAGACTTAT  
TTTCACATGTGGGAGGTTAATCTAGGAATGACTGTTAAGGCCATTTCATGATTCTT  
TGTAGCATTGGTCTGACGTATTATTGTGCTTGTCAAATAATGTTCCCTCCCT  
CATTGTCTGGCGTGTCTGCGTGGACTGGTACGTCAAATCATCCACTGAAA

## FIGURE 28

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45234
><subunit 1 of 1, 453 aa, 1 stop
><MW: 49334, pI: 6.32, NX(S/T): 1
MGENDPPAVEAPFSFRSLFGLDDLKISPVAPDADAVAAQILSLLPLKFFPIIVIGIIALILA
LAIGLGIHFDCSGKYRCRSSFKCIELIARCDGVSDCKDGEDEYRCRVGGQNAVLFVTAAS
WKTMCSDDWKGHYANVACAQLGFPSPYVSSDNLRVSSLEQQFREEFVSIDHLLPDDKVTALHH
SVYVREGCASGHVVTLQCTACGHRRGYSSRIVGGNMSLLSQWPWQASLQFQGYHLCGGSVIT
PLWIITAHCVYDLYLPKSWTIQVGLVSLLDNPAPSHLVEKIVYHSKYKPKR LGNDIALMKL
AGPLTFNEMIQPVCLPNSEENFPDGKVCWTSGWGATEDGGDASPVLNHAAPLISNKICNHR
DVYGGIISPSMLCAGYL TGGVDSCQGDGGPLVCQERRLWKLVGATSGF GIGCAEVNKPGVYT
RVTSFLDWIHEQMERDLKT
```

**Signal Peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 240-284

## **FIGURE 29**

CCCCACGCGTCCGTCTAGTCCCCGGGCAACTCGGACAGTTGCTCATTTATTGCAACGGTCAAGGCCTGGCTTGT  
GCCAGAACGGCGCGCGCGCGCACGCACGACACACACACGGGGGGAAACTTTTTAAAAATGAAAGGCTAGAAGA  
GCTCAGCGCGCGCGCGCTCGCGAGGGCTCCGGAGCTGACTCGCCGAGGCAGGAATCCCTCCGGTCGCGA  
CGCCCGGCCCCGGCTCGCGCCCGTGAGGGATGGTGCAGCGCTGCCGCCGGGGCCGAGAGCTGCTGCACTGAAG  
GCCGGCGACGATGGCAGCGCGCCCGTCCCCGTGCCCCCGCCGCCCTCTGCTGCCCTGGCCGGTGTCT  
GCTCGCGCCCTGCGAGGCCGAGGGGTGAGCTTATGGAACCAAGGAAGAGCTGATGAAGTTGTCACTGCCTCTGT  
TCGGAGTGGGACCTCTGGATCCCAGTGAAGAGCTTCGACTCCAAGAATCATCCAGAAGTGCTGAATATTCGACT  
ACAACGGGAAAGCAAAGAACTGATCATAAATCTGAAAGAAATGAAGGTCTCATGCCAGCTTCACGGAAAC  
CCACTATCTGCAAGACGGTACTGATGTCCTCCCTCGCTGAAATTACACGGTCACTGTTACTACCATGGACATGT  
ACGGGGATATTCTGATTCAAGCAGTCAGTCTCAGCAGTGTCTGGTCTCAGGGGACTTATTGTGTTGAAAATGA  
AAGCTATGTCCTAGAACCAATGAAAAGTGCAACCAACAGATAACAAACTCTTCCAGCGAAGAAGCTGAAAAGCGT  
CCGGGGATCATGTGGATCACATCACACACACAAACCTCGCTGAAAGAATGTGTTCCACCACCTCTCAGAC  
ATGGGCAAGAAGGCATAAAAGAGAGACCCCAAGGCAACTAAGTATGTGGAGCTGGTATCGTGGCAGACAACCG  
AGAGTTTCAGAGGCAAGGAAAAGATCTGAAAAGTTAAGCAGCGATTAATAGAGATTGCTAATCACGTTGACAA  
GTTTACAGACCACTGAACATTCCGATCGTGTGGTAGCGTGGAAACTGTGGAATGACATGGACAAATGCTCTGT  
AAGTCAGGACCCATTCAACAGCCTCCATGAATTCTGGAACCTGGAGGAAGATGAAGGCTTCTACCTCGCAAATCCA  
TGACAATGCGCAGCTGTCAGTGGGTTTATTCCAAGGGACCATCGGCATGGCCCAATCATGAGCATGTG  
CACGGCAGGACAGCTGGGGAAATTGTCATGGACATTCAAGACAATCCCTGGTGCAGCGTGACCCCTGGCACA  
TGAGCTGGGCCACAATTTCGGGATGAATCATGACACACTGGACAGGGCTGTAGCTGTCAAATGGGGTTGAGAA  
AGGAGGCTGCATCATGAAACGCTTCCACCGGGTACCCATTCCCATGGTGTCAAGCAGGAGAAGGACTT  
GGAGAGCAGCCTGGAGAAAAGGAATGGGGTGTGCTGTTAACCTGCCAAGTCAGGGAGTCAGGGAGTCAGGGGGCA  
GAAGTGTGGAAAGACATTGTGAAAGAGGAGAGGTGTGACTGTGGGAGCCAGAGGAATGTATGAATCGCTG  
CTGCAATGCCACCACCTGTACCCCTGAAGCGGACGCTGTGCGCACATGGGCTGTGCTGAAAGACTGCCAGCT  
GAAGCCTGCAGGAACAGCGTGCAGGGACTCCAGCAACTCCGTGACCTCCAGAGTTCTGCACAGGGGCCAGCC  
TCACTGCCAGCCAATGTGACCTGCACGATGGGCACTCATGTCAGGATGTGGACGGTACTGCTACAATGGCAT  
CTGCCAGACTCACGAGCAGCTGTGTCAGCTCTGGGACCAGGTGCTAAACCTGCCCTGGGATCTGTTGA  
GAGAGTCATTCTGCAGGTGATCCTATGGAACACTGTGCAAAGTCTCGAAGAGTTCCATTGCAATGCGAGAT  
GAGAGATGCTAAATGTGAAAATCCAGTGTCAAGGAGGTGCCAGCCGGCCAGTCATTGTTACCAATGCCGTTTC  
CATAGAAACAAACATCCCTCTGCAGCAAGGAGGCCGATTCTGTGCCGGGGACCCACGTGACTTGGCGATGA  
CATGCCGGACCCAGGGTTGTGCTTGCAGGCACAAAGTGTGAGATGGAAAATCTGCCATGCAATGTCATGTC  
AAATATTAGTGTCTTGGGTTCAAGAGTGTGCAATGCACTGCAAGTGTGCAACACAGGAAGAA  
CTGCCACTGCGAGGCCACTGGCACCTCCCTCTGTGACAAGTTGGTTGGAGGAAGCAGACAGCAGGGCC  
CATCCGGCAAGCAGAACAGCAAGGAGGAAGCTGCAGAGTCCAACAGGGAGCGGGCCAGGGCCAGGAGGCCGTGG  
ATCGCAGGAGCATGCGTCACTGCCACTGACACTCATTGAGCCCTCCCATGACATGGAGACCGTGAACCAGTG  
CTGCTGCAGAGGAGGTCAAGCGTCCCCAGGCCTCTGTGACTGGCAGCATTGACTCTGGCTTGCATCGTT  
TCCATGACAACAGACACAACACAGTTCTCGGGCTCAGGAGGGGAAGTCCAGCCTACCGCAGTCTGCAAGAAA  
CACTGCAAGGAAGGGCAGGACTCCCTGGTGTAGCTTGTCAAAACATGGACATGCTTCACTGCTGCTCTGAG  
AGAGTAGCAGGTTACCACTCTGGCAGGGCCAGCCCTGCAGCAAGGAGGAAGAGGACTCAAAGTCTGCCCTTC  
ACTGAGCCTCCACAGCAGTGGGGAGAAGCAAGGGTTGGGCCAGTGTCCCCCTTCCCAAGTGCACACCTCAGCT  
TGGCAGCCCTGATGACTGGTCTCTGGCTGCAACTTAATGCTCTGATATGGCTTTAGCATTTATTATGAAAAT  
AGCAGGGTTTAGTTAATTATCAGAGACCTGCACCCATTCCATCTCCATCCAAGCAAATGAATGGCAA  
TGAAACAAACTGGAGAAGAAGGTAGGAGAAGGGCGGTGAACCTGGCTCTTGCTGTGGACATGCGTGACCAGC  
AGTACTCAGGTTGAGGGTTGCAGAAAGCAGGGACCCACAGAGTCACCAACCCTCATTAAACAAGTAAGAA  
TGTTAAAAGTGAAAACAATGTAAGAGCCTAACTCCATCCCCGTGGCATTACTGCATAAAATAGAGTCATTT  
GAAAT

## FIGURE 30

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49624  
><subunit 1 of 1, 735 aa, 1 stop  
><MW: 80177, pi: 7.08, NX(S/T): 5  
MAARPLPVSPARALLALAGALLAPCEARGVSLWNQGRADEVVSVASVRSGDLWIPVKSFDS  
NIPEVLNIRLQRESKELIINLERNEGLIASSFTETHYLQDGTDVSLARNYTGHCYYHGHVRG  
YSDSAVSLSTCSGLRGLIVFENESYVLEPMKSATNRYKLFPAKKLKVRGSCGSHNTPNLA  
AKNVFPPPSQTWARRHKRETLKATKYVELVIVADNREFQRQGKDLEKVQRLIEIAHVDKF  
YRPLNIRIVLVGVEVWNDMDKCSVSQDPFTSLHEFLDWRKMLLPRKSHDNAQLVSGVYFQG  
TTIGMAPIMSMCTADQSGGIVMDHSDNPLGAAVTLAHELGHNFGMNHDTLDRCCSCQMAVEK  
GGCIMNASTGYPFPMFSSCSRKDLETSLEKGMGVCLFNLPEVRESFGGQKCGNRFVEEGEE  
CDCGEPEECMNRCCNATTCTLKPDAVCAHGLCCEDCQLKPAGTACRDSSNSCDLPEFCTGAS  
PHCPANVYLHDGHSCQDVDGYCYNGICQTHEQQCVTLWGPGAKPAPGICFERVNSAGDPYGN  
CGKVSKSSFAKCEMRDAKCGKIQCQGGASRPVIGTNASVIETNIPLQQGRILCRGTHVYLG  
DDMPDPGLVLAGTKCADGKICLNRQCQNISVFGVHECAMQCHGRGVCNNRKNCCEAHWAPP  
FCDKFGFGGSTDSGPIRQAEARQEAESNRERGQGQEPVGSQEHASTASLTLI

**Signal peptide:**

amino acids 1-28

### FIGURE 31

TCCCAAGGCTTCTTGGATGGCAGATGATTNTGGGGTTTG CATTGTTCCCTGACAACGAAA  
ACAAAACAGTTTGGGGTT CAGGAGGGAAANTCCAGCCTACCCAGGAAGTTGCAGAAACA  
GTGCAAGGAAGGGCAGGANTTCCTGGTTGAGNTTTGNTAAAACATGGACATGNTTCAGTG  
CTGCTCNTGAGAGAGTAGCAGGTTACCAC TTTGGCAGGCCAGCCCTGCAGCAAGGAGGA  
AGAGGACTCAAAGTTGGCCTTCACTGAGCCTCCACAGCAGTGGGGAGAAGCAAGGGTT  
GGGCCAGTGTCCCCTTCCCCAGTGACACCTCAGCCTGGCAGCCCTGATAACTGGTNTNT  
GGCTGCAANTTAATGCTNTGATATGGCTTTAGCATTATTATATGAAAATAGCAGGGTTT  
AGTTTTAATTATCAGAGACCCTGCCACCCATTCCATNTCCATCCAAG

## **FIGURE 32**

CATCCTGCAACATGGTGAACACCACGCCGGCTAATTTGTTGTATTTGGTAGAGATGGGA  
TTTCACCGTGTAGCCAGGATTGTCTCAATCTGACCTCATGATCTGCCCGCTCGGCCTCCC  
AAAGTGCTGGATTACAGGCAGTGCAACCACACCGGCCACAAACTTTAAGAAGTTAAT  
GAAACCATACTTTACATTTAATGACAGGAAAATGCTACAATAATTGTTAACCCAAA  
TTCTGGATACAAAAGTACAATCTTACTGTGTAAATACATGTATATGTACTATATGAAAATA  
TACCAAATATCAATAACTTATCTCTGGTAAAAACCTCTTCATACCCGTGCTAACAA  
CTTTAACAAAAAATTCATCACTTTAAGAATCAAGAAAATTCATGAAGGTATATGGG  
ACAGAAAAAAACCAAGGGAAAATCACGCCACTTGGGAAAAAGATTGAAATCTGCCT  
TTTTATAGATTGTAATTAATAAGGTCCAGGCTTCTAAGCAACTTAAATGTTGTTCGA  
AACAAAGTACTTGTCTGGATGTAGGAGGAAAGGGAGTGTACTGCCATTATGATGCC  
TTGAATATAAGACCCACTTGCTATCTCCCTGCACCAGCCAGGAGCCACCCATCCTCCAGC  
ACACTGAGCAGCAAGCTGGACACACGGCACACTGATCAAATGGTAAGGGATGGTGGCGA  
TGCTCATTCTGGGTCTGCTACTTCTGGCGCTGCTCCTACCCGTGCAGGTTCTTCATTGTT  
CCTTAACCAGTATGCCGGAAAGCTACTGCAGCCAAACACAAAGCCCTCCAACAGTGCC  
ACAGCCTACAGCCGGTCTCCTGTGGCTTGCTTGCCTTCTACATCTTACCATTAAGAGG  
CAGGTCAAGAACAGCTACAGTTCTCCAACCCATACACTAAACCGAATCCAAATGGTGC  
AGAAGTTCAATGTGGCAAGGAAAAAACAGGTCTTCATCAAATCTACTAATTCACTC  
ATTAACAGAGAAACGCTTGAGAGTCTCAAACGGACTGGTTAAAGAGCATCTGAAGGATT  
GACTAGATGATAATGCCGTACTCCAGTACTTGGAGGCCCTAGGCCGGGATCACCTG  
AGGTCAAGGAGTTGAGACTAACCTGCCAAATGGTGAACCCATCTGTACTAAAAATACA  
AATATTGACTGGCGTGGTGGTGAGTGCCTGTGATCCAGCTACTCAGGTGGCTGAAGCAGG  
ACAATCACTGAACTCAGGAGGCAGAGGTTGCAGTGAGCTGAGATCGCGCTACTGCACTCTA  
GCCTAGCCTGGCAACAGAGTGAGACTCGTCTCAAAAAAAAAAGCCAAGTGCAGTGGCT  
CACGCCGTAAATCCGGCAGTGGAGGCCAGGTGGCGGATCACGAGGTAGGAGATCA  
AGACCACCTGGCTAATACAGTGAACCCGTCTACTAAAAATACAAAAATTAGCC  
GATGGTGGCAGGCACCTGGAGTCCAGCTACTCGGGAGGCTGAGGCAGGAGAATAGCGT  
CTCAGGAGGCGGAGCTTGCACTGAGCCGAGATTGCGCTACTGCACCTCCAGCCTGGCGACAG  
CGCGAGACTCCGTCTAAAAAAAAAAAAAA

## FIGURE 33

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48309
><subunit 1 of 1, 67 aa, 1 stop
><MW: 6981, pI: 7.47, NX(S/T): 0
MGKGMVAMLILGLLLLALLLPVQSSFVPLTSMPEATAAETTKPSNSALQPTAGLLVVLLAL
LHLYH
```

**Signal peptide:**

amino acids 15-27

## FIGURE 34

GCCGGCGGAGAGCGCGCCAGCCCCGCCGATGCCCGCGCCAGGACGCCCTCCGCTGCTGGCCCGC  
CGGCGGGCTGACTGCGCTGCTGCTGCTGGGCCATGGCGGCGGGCGCTGGGCAGGGCCAGGAGCACC  
AGGCGGGGGCGGGCGGGCGAGGGCCCCCGCGCAGACGGGAGGACGGACAGGACCCGACAGCAAGCACC  
TGTACACGGCCGACATGTTACGCACGGGATCCAGAGCGCCGCGCACTTCGTCATGTTCTCGGCCCTGGTGTG  
GACACTGCCAGCGGCTGCAGCCACTTGAATGACCTGGGAGACAAATAAACAGCATGGAAGATGCCAAGTCT  
ATGTTGGCTAAAGTGGACTGCACGGCCACTCCGACGTGTGCTCCGCCAGGGGGTGCAGGATACCCACCTTAA  
AGCTTTCAAGCCAGGCCAAGAAGCTGTGAAGTACCCAGGGACTTCAGACACTGGAAAAGTGGATGC  
TGCAGACACTGAACGAGGAGCCAGTGACACCAGGCCAGTGGAACGCCAGTGCCCCGAGCTCAAGCAAG  
GGCTGTATGAGCTCAGCAAGCAACTTTGAGCTGCACGTTGCACAAGGCAGCACCTTATCAAGTCTCGCTC  
CGTGGTGTGGTCACTGCAAAGCCCTGGCTCCAACCTGGGAGCAGCTGGCTCTGGGCCCTGAAACATTCCGAAACTG  
TCAAGATTGCAAGGGTGTACACAGCAGTGAACCTCTGCTCCGGAAACAGGGTGTGGCTATCCCACTC  
TTCTCTGGTTCGGAGATGGGAAAAAGGGTGGATCAGTACAAGGGAAAGCAGGGATTGGAGTCAGTGGAGTAGC  
TGGAGCTGCCAGCTGCAGCGCACAGAGACTGGAGCAGGGAGACCTCACGCCCTCAGAGGCCCCGGTCTGGCAG  
CTGAGGCCAGGGCTGACAAGGGCAGTGTGTTGCCACTCACTGAAAATAACCTCGATGACACCATTGAGAAGGAA  
TAACCTTCATCAAGTTTATGCTCCATGGTGTGGTCAATTGTAAGACTCTGGCTCCTACTTGGGAGGAACCTCTCTA  
AAAAGGAATTCCCTGGTCTGGGGGGTCAAGATGCCAGTGAAGTACAGTGCACACTGCTGAACGGAAATATCTGAGCA  
AGTATTGGTACGAGGCTACCCCCACGTTATTGCTTTCCGAGGGAGGAAGAAAGTCAGTGAGCACAGTGGAGGCA  
GAGACCTTGACTCGTTACACCGCTTGTCTGAGCCAAGCGAAAGACGAACTTTAGGAACACAGTTGGAGGTAC  
CTCTCTGCCAGCTCCGCACCCCTGGCTTAGGAGTTAGTCACTCCACAGAGGCCACTGGGTTCCAGTGGTGGCT  
GTTCAGAAAGCAGAACATACAGCTGAGGTATCTCTTGTTGTTGAGGAAACACACTCTACAG  
ATTCTTTATTAAGTTAAAGTTCTCAAGTAAATGTGTAACTCATGGTCACTGTGAAACACATTTCAGTGGCGATA  
TATCCCCTTGACCTTCTCTGATGAAATTACATGGTTCCCTGAGACTAAAATAGCGTTGAGGGAAATGAAA  
TTGCTGGACTATTGTTGGCTCTGAGTTGAGTTGAGTTGGTGAAGAAAGAACATCCAAGCATAGTTACCTGC  
CCACGAGTTCTGGAAAGGTGGCCTGTGGCAGTATTGACGTTCTCTGATCTTAAGTCACAGTTGACTCAAAAC  
TGTGTTGGTCCGTAGCATGGAGCAGATTGAAATGAAAAACACACCTCTGGAGATAACCTTCAGGCCGCTG  
TGGAGCTCTGTTGCTGTGAATACCTCTCAGTGTGAGAGGTTAGCCGTGATGAAAGCAGCGTACTCTGACC  
GTGCCTGAGTAAGAGAATGCTGATGCCATAACTTATGTCGATACTTGTCAAAACTGTTACTGTTGAGGGAT  
CCTTCTGTTCTCACGGGGTGAACATGCTTCTGAGGAAACACACTGTTAACACGAAGCAGGCCACATGAACTGT  
TGGATGCTTCTCTAGAAAGGGTAGGAGTGGAAATTCCACCGAGGCTATTCTCAGTATCTCATTAACCTATTGA  
AAGATTCCAGTTGATTGTCACCTGGGTGACAAGACCCAGACAGGCTTCCAGGCCGGTATCCAGGGAGG  
TCTGCAGCCCTGCTGAAGGGCCCTAACTAGAGTTCTAGAGTTCTGATTCTGTTCTCAGTAGTCCTTTAGAGG  
CTTGCTATACTTGTCTGCTCAAGGAGGTGACCCCTTAATGTTGAGAATGGGATGCAATTGATCTCAAGAC  
CAAAGACAGATGTCAGTGGGCTCTGGCCCTGGTGTGACGGCTGTGGCAGCTGGTGTGAGTCAGTGTCTCTA  
ACTCATGTCGTCCTTGTGATTAACACCTCTATCTCTCTGGGAAATAAGCACACATACAGGTTAGCTCAAGATA  
GATAGGTGTTGTCCTTTACCATGAGCTACTTCCCATAATAACCACTTGCATCCAACACTCTCACCCACCT  
CCCACAGCAAGGGGATGTGGATACTTGGCCAAAGTAACTGGTGGTAGGAATCTTAGAAACAAGACCAACTTATA  
CTGTCGTCTGAGGCAGAAGATAACAGCAGCATCTGACCAGCCTCTGCCCTAAAGGAATCTTATTAATCAG  
TATGGTTACAGATAATTCTTTTAAAGGAACACCTCTAGAGAAGCACAACGTCAAGAGTCTTGTACA  
CACAACTTCAGCTTGTCATCACAGAGTCTGTATTCCAAGAAAATCAAAGTGGTACAATTGTTGTTACACTAT  
GATACTTCTAAATAAAACTCTTTTTTTAA

## FIGURE 35

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA46776
><subunit 1 of 1, 432 aa, 1 stop
><MW: 47629, pi: 5.90, NX(S/T): 0
MPARPGRLLPPLLARPAALTALLLLLGHGGGGRWGARAQEAAAAAADGPPAADGEDGQDPHS
KHLYTADMFTHGIQSAAHFVMFFAPWCGHCQRLQPTWNNDLGDKYNNSMEDAKVYVAKVDCTAH
SDVCSAQGVRGYPTLKLFKPGQEAVKYQGPRDFQTLENWMLQTLNEEPVTPEPEVEPPSAPE
LKQGLYELSAASNFEHLVAQGDHFIKFAPWCGHCKALAPTWEQLALGLEHSETVKIGKVDCT
QHYELCSGNQVRGYPTLLWFRDGKKVDQYKGKRDLESLEYVESQLQRTEGATETVTPSEA
PVLAEEPEADKGTVLALTENNFDITIAEGITFIKFYAPWCGHCKTLAPTWEELSKKEFPGLA
GVKIAEVDCATAERNICSKYSVRGYPTLLLFRGGKKVSEHSGGRDLDLHRFVLSQAKDEL
```

**Signal sequence:**

amino acids 1-32

## FIGURE 36

CTTTCTGAGGAACCACAGCAATGAATGGCTTGATCCTGCTTCGAAGAAACCAATTAT  
CCTCCTGGTACTATTCTTTGCAAATTCAAGACTGGGTCTGGATATTGATAGCCGTCTA  
CCGCTGAAGTCTGTGCCACACACACAATTCAACAGGACCCAAAGGAGATGATGGTAAAAA  
GGAGATCCAGGAGAAGAGGGAAAGCATGGCAAAGTGGACGCATGGGGCCGAAAGGAATTAA  
AGGAGAACTGGGTGATATGGGAGATCAGGGCAATATTGGCAAGACTGGCCCATTGGGAAGA  
AGGGTGACAAAGGGAAAAAGGTTGCTGGAATACCTGGAGAAAAAGGCAAAGCAGGTACT  
GTCTGTGATTGTGGAAGATAACCGGAAATTGTTGACAACACTGGATATTAGTATTGCTCGGCT  
CAAGACATCTATGAAGTTGTCAAGAATGTGATAGCAGGGATTAGGAAACTGAAGAGAAAT  
TCTACTACATCGTGCAGGAAGAGAAGAACTACAGGAATCCCTAACCCACTGCAGGATTGG  
GGTGGAAATGCTAGCCATGCCAAGGATGAAGCTGCCAACACACTCATCGCTGACTATGTTGC  
CAAGAGTGGCTTCTTCGGGTGTTCAATTGGCGTGAATGACCTGAAAGGGAGGGACAGTACA  
TGTCCACAGACAACACTCCACTGCAGAACTATAGCAACTGGAATGAGGGGGAACCCAGCGAC  
CCCTATGGTCATGAGGACTGTGTGGAGATGCTGAGCTCTGGCAGATGGAATGACACAGAGTG  
CCATCTTACCATGTACTTGTCTGTGAGTTCAAGAAGAAAAGTAACTTCCCTCATCCT  
ACGTATTCGCTATTTCTGTGACCGTCATTACAGTTATTGTTATCCATCCTTTTCTG  
ATTGTACTACATTGATCTGAGTCAACATAGCTAGAAAATGCTAAACTGAGGTATGGAGCCT  
CCATCATCAAAAAAAAAAAAAAAA

## FIGURE 37

```
>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50980
><subunit 1 of 1, 277 aa, 1 stop
><MW: 30645, pI: 7.47, NX(S/T): 2
MNGFASLLRRNQFILLVLFLLQIQSLGLDIDSRPTAEVCATHTISPGPKGDDGEKGDPGEEG
KHGKVGRMGPKGIKGELGDMGDQGNIKGKGPPIGKKGDKGEKGLLGIPEKGKAGTVCDGRY
RKFGVQLDISIARLKTSMKFVKNVIA吉IRETEEKFYIVQEEKNYRESLTHCRIRGGMLAMP
KDEAANTLIADYVAKSGFFRVFIGVNLDEREGQYMSTDNTPLQNYSNWNEGEPSDPYGHEDC
VEMLSSGRWNDTECHLTMYFVCEFIKKKK
```

**Signal peptide:**

amino acids 1-25

## **FIGURE 38**

GGTTCTATCGATTGAATTCGCCACACTGGCCGGATCCTCTAGAGATCCCTCGACCTCGAC  
CCACCGTCCGCTCTCCGCCGTGGAGTGGTGGGGCTGGTGGGAATGGCGTGT  
GCCAGCGCACGCGCCTCCCTGGAAGGAGAAGTCTCAGCTAGAACGAGCGGCCCTAGGTTT  
CGGAAGGGAGGATCAGGGATGTTGCAGCGGCTGGAACCAGACGGTGCCATAGAGGAAGC  
GGGCTCCATGGCTGCCCTCTGCTGCTGCCCTGCTGCTGTTGCTACCGCTGCTGCTGCTGA  
AGCTACACCTCTGCCGCAGTTGCCTGGCTCCGGGACTTGGCTTGCGGCTGCCGAGCT  
CTGTGCTGCAAAGGGCTTCAGCTCGGCCCTGGCCGGCTGCCGCCGACCCGAAGG  
TCCCGAGGGGGCTGCAGCTGGCCTGGCGCTCGCGAACACTGGCCAGCAGCGGCCGCG  
ACACCTTCTCATTCACGGCTCGCGCCTTAGCTACTCAGAGGCGGAGCGCAGAGTAAC  
AGGGCTGCACGCCCTCCTACGTGCCTAGGCTGGACTGGGACCCGACGGCGCGACAG  
CGCGAGGGAGCGCTGGAGAAGGCGAGCGGGCAGCGCCGGAGCCGGAGATGCAGCGGCC  
GAAGCGCGCGGAGTTGCCGGAGGGACGGTGCCTGGCGCAGAGTGGAGGAGCCGCC  
CTGTCACCTGGAGCAACTGTGGCGCTGCTCCTCCCCGCTGGCCAGAGTTCTGTTGCT  
GTTGGGCTGGCCAAGGCCGCTGCCACTGCCCTTGTGCCAACGCCCTGCCGGGCC  
CCCTGCTGCACTGCCCTCGCAGCTGCCCGCGCTGGTGCCTGGCCAGAGTTCTG  
GAGTCCTGGAGCCGGACCTGCCGCTGAGAGCCATGGGCTCCACCTGTGGCTGCAGG  
CCCAGGAACCCACCCCTGCTGGAATTAGCATTGCTGGCTGAAGTGTCCGCTGAAGTGGATG  
GGCCAGTGCCAGGATACTCTCTTCCCCCAGAGCATAACAGACACGTGCCTGTACATCTC  
ACCTCTGGCACCACGGCCTCCCAAGGCTGCTGGATCAGTCATCTGAAGATCCTGCAATG  
CCAGGGCTCTATCAGCTGTGGTCCACCAGGAAGATGTGATCTACCTGCCCTCCCAC  
TCTACCACATGTCCGGTCCCTGCTGGCATCGTGGCTGCATGGCATTGGCACAGTG  
GTGCTGAAATCCAAGTTCTGGCTGGTCAAGTCTGGGAAGATTGCCAGCACAGGGTGC  
GGTGTCCAGTACATTGGGAGCTGTGCCATACCTGTCAACCAGCCCCGAGCAAGGCAG  
AACGTGGCCATAAGGTCCGGCTGGCAGTGGCAGCGGGCTGCCAGATACTGGAGCGT  
TTTGTGGCGCTCGGGCCCTGCAGGTGCTGGAGACATATGACTGACAGAGGCAACGT  
GGCCACCATCAACTACACAGGACAGCGGGCGCTGTGGGCGTGTCTGGCTTACAAGC  
ATATCTTCCCTTCTCCTTGATTGCTATGATGTCACCACAGGAGAGCCAATTGGGACCC  
CAGGGGCACTGTATGCCACATCTCAGGTGAGCCAGGGCTGCTGGTGGCCCCGTAAGCCA  
GCAGTCCCCATTCTGGCTATGCTGGCGGCCAGAGCTGGCCAGGGAAAGTTGCTAAAGG  
ATGTCTTCCGGCTGGGATGTTTCTCAACACTGGGACCTGCTGGCTGCGATGACCAA  
GGTTTCTCCGCTTCCATGATCGTACTGGAGACACCTCAGGTGGAAGGGGAGAATGTGGC  
CACAACCGAGGTGGCAGAGGTCTCGAGGCCCTAGATTTCTCAGGAGGTGAACGTCTATG  
GAGTCACTGTGCCAGGGCATGAAGGCAGGGCTGGAATGGCAGCCCTAGTCTGCGTCCCC  
CACGCTTGGACCTTATGCACTACACCCACGTGCTGAGAACCTGCCACCTTATGCCCG  
GCCCGATTCTCAGGCTCCAGGAGTCTTGGCCACCACAGAGACCTCAAACAGCAGAAAG  
TTCGGATGGCAAATGAGGGCTCGACCCAGCACCTGCTGACCCACTGTACGTTCTGGAC  
CAGGCTGTAGGTGCCTACCTGCCCTACAACACTGCCGGTACAGCGCCCTGGCAGGAAA  
CCTTCGAATCTGAGAACCTCACACCTGAGGCACCTGAGAGAGGAACCTGTGGGGTGGGG  
CCGTTGCAGGTGTACTGGGCTGTCAGGGATCTTCTATACCAGAACCTGCGGTCACTATT  
GTAATAATGTGGCTGGAGCTGATCCAGCTGCTCTGACCTAAAGGGGGGGGGGGGGGG  
AAAAAAAAAGGGCGGCCGCACTAGAGTCGACCTGCAGTAGGGATAACAGGGTAATAAGC  
TTGGCCGCCATGGCCAACCTGTTATTGCAG

## FIGURE 39

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50913  
><subunit 1 of 1, 730 aa, 1 stop  
><MW: 78644, pI: 7.65, NX(S/T): 2  
MGVCQRTRAPWKEKSQLERAALGFRKGSGMFASGWNQTVPIEEAGSMAALLLPLLLLLPL  
LLLKLHLWPQLRWLPAIDLAFAVRALCCKRALRALARAAAAADPEGPEGGCSLAWRLAELAQ  
RAAHTFLIHGSRRFSYSEAERESNRAARAFLRALGWDWGPDDGDSGEGSAGEGERAAPGAGD  
AAAGSGAEFAGGDGAARGGGAAAPLSPGATVALLLPAGPPEFLWLWFGLAKAGLRTAFVPTAL  
RRGPLLHCLRSCGARALVLAPEFLESLEPDLPALRAMGLHLWAAGPGTHPAGISDLLEAVSA  
EVDPVPGYLSSPQSITDTCLYIFTSGTTGLPKAARIHLKILQCQGFYQLCGVHQEDVIYL  
ALPLYHMSGSSLGIVGCMGIGATVVLKSKFSAGQFWEDCQQHRVTVFQYIGELCRYLVNQPP  
SKAERGHKVRLAVGSGLRPDTWERFVRRFGPLQVLETYGLTEGNVATINYTGQRGAVGRASW  
LYKHIFPFSLIRYDVTTGEPIRDPOGHCMATSPGEPLLAVPVSQQSPFLGYAGGPELAQGK  
LLKDVFVFRPGDVFFNTGDLLVCDQGFLRFHDRTGDTFRWKGENVATTEVAEVFEALDFLQE  
NVYGVTVPGHEGRAGMAALVLRPPHALDLMQLYTHVSENLPYARPRFLRLQESLATTEFK  
QQKVRMANEGFDPSLSDPLVLDQAVGAYLPLTTARYSALLAGNLRI

**Type II transmembrane domain:**

amino acids 45-65

**Other transmembrane domain:**

amino acids 379-398

**cAMP- and cGMP-dependent protein kinase phosphorylation site**  
starting at amino acid 136

**CUB domain protein motif**

amino acids 254-261

**putative AMP-binding domain siganture**

amino acids 332-343

**N-glycosylation sites**

amino acids 37-40 and 483-486

## **FIGURE 40**

CCTGTGTTAAGCTGAGGTTCCCTAGATCTGTATATCCCCAACACATACTCCACGCACA  
CACATCCCCAAGAACCTCGAGCTCACACCAACAGACACACGCGCGCATACACTCGCTCTC  
GCTTGTCCATCTCCCTCCCAGGGAGCCGGCGCGCTCCCACCTTGCCGCACACTCCGGC  
GAGCCGAGCCCGCAGCGCTCAGGATTCTCGCGCTCGGAACTCGGATTGCAGCTCTGAACCC  
CCATGGTGGTTTTAAACACTTCTTCTCTCGTTGATTGCACCGTTCCA  
TCTGGGGCTAGAGGAGCAAGGCAGCAGCCTCCCAGCCAGGCCCTGGCTGCCATCGT  
CCATCTGGCTTATAAAAGTTGCTGAGCGCAGTCAGAGGGCTGCGCTGCTCGTCCCCTCGG  
CTGGCAGAAGGGGTGACGCTGGCAGCGCGAGGAGCGGCCGCTGCCTCTGGCGGGCTTT  
CGGCTTGAGGGCAAGGTGAAGAGCGCACCGCCGTGGGTTACCGAGCTGGATTGTATG  
TTGCACCATGCCTTCTTGATCGGGCTGTGATTCTCCCTTTGGGCTGCTGCTCTCCC  
TCCCCGCCGGGGCGATGTGAAGGCTCGGAGCTCGGGAGAGGTCCGCCAGCGTACGGTGCC  
AAGGGATTAGCCTGGCGGACATCCCCTACCAAGGAGATCGCAGGGAACACTTAAGAATCTG  
TCCTCAGGAATATAACATGCTGCACCACAGAAATGGAAGACAAGTTAACGCAACAAAGCAAAC  
TCGAATTGAAAACCTTGTGGAAGAGACAAGCCATTTGTGCGCACCACTTTGTGTCCAGG  
CATAAAGAAATTGACGAATTTCGAGAGCTCTGGAGAATGCAGAAAAGTCACTAAATGA  
TATGTTGTACGGACCTATGGCATGCTGACAGAATTCAAAGTCTTCAGGACCTCT  
TCACAGAGCTGAAAAGGTACTACACTGGGGTAATGTGAATCTGGAGGAAATGCTCAATGAC  
TTTGGGCTCGGCTCTGGAACGGATGTTAGCTGATAAACCTCAGTATCAGTGA  
AGACTACCTGGAATGTGAGCAAATACACTGACCAGCTCAAGCCATTGGAGACGTGCC  
GGAAACTGAAGATTAGCTGAGTTACCCGCGCTTCATTGCTGCCAGGACCTTGTCCAGGGCTG  
ACTGTGGGAGAGAAGTTGCAAACCGAGTTCCAAGGTCAAGCCAAACCCAGGGTGTATCCG  
TGCCTCATGAAGATGCTGTACTGCCATACTGTCGGGGCTTCCACTGTGAGGCCCTGCA  
ACAACACTGTCTAACGTCAAGGGCTGTTGCAAATCAGGCTGACCTGACACAGAG  
TGGAATCTGTTATAGATGCAATGCTCTGGTGGCAGAGCGACTGGAGGGCATTCAACAT  
TGAGTCGGCATGGACCCGATAGATGTCAGAAGATTCTGAAGCCATTATGAACATGCAAGAAA  
ACAGCATGCAGGTGCTGCAAAGGTCTTCAGGGATGTGGTCAGCCAAACCTGCTCCAGCC  
CTCAGATCTGCCGCTCAGCTCTGAAAATTAAATACACGTTCAAGGCCCTACAATCCTGA  
GGAAAGACCAACAACGCTGCAGGACAAGCTGGACCGGCTGGTCACAGACATAAAAGAGA  
AATTGAAGCTCTAAAAAGGTCTGGTCAGCATTACCTACACTATCTGCAAGGACGAGAGC  
GTGACAGCGGGCACGTCCAACGAGGGAGGAATGCTGGAACGGGCACAGCAAAGCCAGATACTT  
GCCTGAGATCATGAATGATGGCTCACCAACCAGATCAACAATCCGAGGTGGATGTGGACA  
TCACTCGGCTGACACTTCATCAGACAGCAGATTATGGCTCTCCGTGTGATGACCAACAAA  
CTAAAAAAACGCCTACAATGGAATGATGTCAATTCCAGGACACAAGTGTGACCAATCCAGTGG  
CTCAGGGAGTGGCAGTGGGTGCATGGATGACGTGTGTCACGGAGTTGAGTTGTGACCA  
CAGAGGCCCGCAGTGGATCCGACCGGAGAGAGGGTGGACTCTCTGCAGCCAGCGTGGC  
CACTCCCTGCTCTGGTCTCTCACCTGCATTGTCCTGGCACTGCAGAGACTGTGAGATA  
ATCTTGGGTTTGTCAGATGAAACTGCATTAGCTATCTGAATGGCCAACACTCACTTCTT  
TTCTTACACTCTGGACAATGGACCATGCCACAAAAACTTACCGTTCTATGAGAAGAGAG  
CAGTAATGCAATCTGCCTCCCTTTGTTTCCAAAGAGTACCGGGTGCAGACTGAACG  
CTTCCTCTTCCTCAGCTATCTGTGGGGACCTTGTATTCTAGAGAGAATTCTTACTCAA  
ATTTTCTGTAACGAGGAGATTCTTACCTTCATTGCTTTATGCTGCAGAAGTAAAGGAAT  
CTCACGTTGTGAGGGTTTTCTCATTAAAAT

## FIGURE 41

>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50914  
><subunit 1 of 1, 555 aa, 1 stop  
><MW: 62736, PI: 5.36, NX(S/T): 0  
MPSWIGAVILPLLGLLSLPAGADVKARSCGEVRQAYGAKGFSLADIPYQEIA  
GEHLRICPQEYTCCTTEMEDKLSQQSKLEFENLVEETSHFVRTTFVSRHKKFDEFF  
RELLENAEKS LNDMF VRTYGMLYMQNSEVFQDLFTELKRYYTGGVNLEEMLNDFWAR  
LLERMFQLINPQYHFSEDY LECVSKYTDQLKPFGDVPRKLKIQVTRAFIAARTFVQGLTVG  
REVANRVSKVSPTPGCIRAL MKMLYCPYCRGLPTVRPCNNYCLNVMKCLANQADLD  
TEWNLFIDAMLLVAERLEGPFNIES VMDPIDVKISEAIMNMQMENSMQVS  
AKVFQGCGQPKPAPALRSARSAPENFNTRFRPYNPEER PTTAAGTSLDRLVT  
DIKEKLKLSKKVWSALPYTICKDESVTAGTSNEEECWNGHSKARYLPE IMNDGLTN  
QINNPEVDVDITRPDTFIRQQIMALRVMTNKLKNAYNGNDVNFQDTSDESGSG  
SGSGCMDDVCPTEFEFVTTEAPAVDPDRREVDSSAAQRGHSLLSWSLTCIVL  
ALQRLCR

**Signal peptide:**

amino acids 1-23

## **FIGURE 42A**

CGGACGCGTGGCGGACCGTGGCAAAAGAACCTGGAGTGCAAAGCTAAATAAGTTAGCTGAGAAAACGCACG  
CAGTTGCAGCGCCTGCGCCGGGTGCGCCAACCTACGCAAAGACCAAGCGGGCTCCGCGCGGACCGGCCGGGGC  
TAGGGACCCGGCTTGGCCTTCAGGCTCCCTAGCAGCGGGAAAAGGAATTGCTGCCCGAGTTCTGCGGAGGT  
GGAGGGAGATCAGGAAACGGCTTCTCCTCACTTCGCCCCGTGGTGAGTGTGCGGGAGATTGGCAAACGCCTAGG  
AAAGGACTGGGAAAATAGCCCTGGAAAGTGGAGAAGGTGATCAGGAGGCGGTCCACTACGGCAGTTATCTG  
TCTGATCAGAGCCAGACCGCACGCGTCCACTTCGAGTTCTTCAGGTGAGTGGGACCGCAGGACAGACGGCGA  
TCCCGCCGCCCTCCGTACCAGCACTCCCAGGAGAGTCAGCCTCGCTCCCAACGTCGAGGGCGCTCTGCCACGA  
AAAGTTCCGTCCACTGTGATTCTCAATTCCCTGCTTGGTTTTCTCCAGAGAACTTTGGTGGAGATATTAA  
ACTTTTTCTTTTTCTGGTGGAAAGCTGCTCTAGGAGGGGGAGGAGGAGGAGAAAGTGAATGTGC  
TGGAGAAGAGCGAGCCCTCCTGTTCTCCGGAGTCCCATTAAAGCATCATTCTGAAAGATTAAAGTTGT  
CGGACATGGTGACAGCTGAGAGGAGAGGAGGAGTTCTGCAAGGTGGAGAGTCCTCACCGTCTGGTGCATG  
TGTGCGCCCGCAGCGGGCGGGCGTGGTCTCCGCGTGGAGTCTCACCTGGACCTGAGTGAATGGCTCCCA  
GGGGCTGTGCGGGGCATCCGCTCCGCTTCTCCACAGGCCTGTGTCTGGAAAGATGCTAGCAATGGGG  
CGCTGGCAGGATTCTGGATCCTCTGCCTCCTCACTTATGGTACCTGTCCTGGGCCAGGCCTAGAAGAGGAGG  
AAGAAGGGCCTTAAGCTCAAGCTGGAGAGAACTAGAGCCAGCACAACTTCCACCTCCAGCCCCATCTCA  
TTTCATCCTAGGGATGATCAGGAGTTAGAGATGTGGTTACCA CGGATCTGAGATTAAAACACCTACTCTG  
ACAAGCTCGCTGCCGAAGGAGTTAACTGGAGAACTACTATGTCCAGCCTATTGCAACACCATCCAGGAGTCAGT  
TTATTACTGGAAAGTATCAGATAACACCCGGACTTCACATTCTATCATAAGACCTACCAACCCAACTGTTAC  
CTCTGGACAATGCCACCCACCTACAGAAACTGAAGGAGGTGGATATTCAACGCAATGGTCGGAAAATGGCACT  
TGGGTTAACAGAAAAGAATGCATGCCACCAAGAGGAGTTGATACTTTGGTTCCCTTTGGGAAGTG  
GGGATTACTATACACACTACAAATGTGACAGTCTGGATGTGTGGCTATGACTGTATGAAACGACAATGCTG  
CCTGGACTATGACAATGGCATATACTCCACACAGATGTACACTCAGAGAGTACAGCAAATCTAGCTCCATA  
ACCCCAAAAGCTATATTTTATATACTGCCTATCAAGCTGTTCACTCACCAGTCAAGCTCCTGGCAGGTATT  
TCGAACACTACCGATCCATTATCAACATAAACAGGAGAAGATATGCTGCCATGCTTCTGCTTAGATGAAGCAA  
TCAACAAACGTGACATTGGCTCTAAAGACTTATGGTTCTATAACAACAGCATTATCATTACTCTCAGATAATG  
GTGCCAGCCTACGGCAGGAGGAGTAACCTGGCTCTCAGAGGTAGCAAAGGAACATATTGGGAAGGAGGGATCC  
GGGCTGTAGGCTTGTGCATAGCCCACCTCTGAAAAACAAGGAACAGTGTGTAAGGAACATTGTGCACATCACTG  
ACTGGTACCCACTCTCATTCACTGGCTGAAGGACAGATTGATGAGGACATTCAACTAGATGGCTATGATATCT  
GGGAGACCATAAGTGGGTCTCGCTCACCCGAGTAGATATTGCTACATTGACCCCTACACCAAGGC  
AAAAAAATGGCTCTGGCAGCAGGCTATGGATCTGAAACACTGCAATCCAGTCAGCCATCAGAGTGCAGCACTG  
GAAATTGCTTACAGGAAATCCTGGCTACAGCAGTGGTCCCCCTCAGTCTTCAGCAACCTGGACCGAACCG  
GTGGCACAATGAACGGATCACCTGTCAACTGGCAAAAGTGTATGGCTTCTCAACATCACAGCCACCCATATGA  
GAGGGTGGACCTATCTAACAGGTATCCAGGAATCGTGAAGAAGCTCCTACGGAGGCTCTCACAGTTCAACAAAC  
TGCAGTGCCTGGTCACTGGTCAAGGACTTCTGCAAGGACAGTGGAGATGTTATTCTCGCTCCTTAGAAAACGTG  
GTGAGTCCTGAGTTCCACTGCTGTGCTTCAGTCACAGCAGGAAACACTGCTTTGAATTATAGGAGGAGAACATA  
ACCTACCATCCGCAAGCATGCTAATTGATGGAAGTTACAGGGTAGCATGATTAAACTACCTTGATAAATTAC

## **FIGURE 42B**

AGTCAAAGATTGTGTCACCTCAAAGGCCTGAAGAATATATTTCTGGTGAATTTGTATGTCTGTCATATGA  
CACTGGGTTTTAATTAAATTCTATTTATATATAAATATGTTCTTCCTGTGAAAAGCTGTTTCT  
CACATGTGAACAGCTTGACACTCATTTACCATGCGTGAGGGAATGGCAAATAAGATGTTGAGCACACTGCC  
ACAATGAATGTAACATTTCTAACACTTTACTAGAAGAACATTCACTGATAAAAAACCTAATTTATTTACA  
GAAAAATATTTGTTGTTTATAAAAGTTATGCAAATGACTTTATTTTATTCCTGCATACCATTAGAAGA  
ATTTTATTCATTCTCAAATTATCAAGCACTGTAATACTATAAATTATGTAATACTGTGTGAATTCACTGACTA  
TAAAAACATCATTCACTGAGAAACTTATAATCGCATTGTCATCAAGATTGAAATGTAATAAGATGAATATAT  
ATTACTGGAAATTCAATGTTGTCAGAGTTGAGACAACTTATTGTTCTATCATAAACTATTTATGTATCTT  
AATTATTAAAATGATTACTTTATGGCACTAGAAAATTACTGTGGCTTCTGATCTAACCTCTAGCTAAATT  
GTATCATTGGCCTAAAAAATAAAAACTTTACTAATAGGCAATTGAAGGAATGGTTGCTAACACCACAGTAA  
TATAATATGATTACAGATAGATGCTTCCCCTGGCTATGACATGGAGAAAGATTTCCATAATAAACTAA  
TATTTATATTAGGTTGGTCAAAACTAGTTGCGGTTTCCATTAAAAGTAATAACCTTACTCTTATACAAAGT  
GGACACTGTGGGAGATAAGAGAAATGGAAGATA CGGATCCTGCCTGGAGTAGGTAACCTGCTGGAAACCCC  
ACATGCAAACGTATGAGGAGATTAAAGGAGTATTATCAGTAATGAAGTTATCATGGTCATCAATGAGCATA  
GATTGGTGTGGATCCTGTAGACCCTGGTGTTCCTTGAAGTGCCCTCTCTAATGCAGAGCCTGAAAGCTTAC  
AGTATAACACTGAAAAGTCACAGATAGCTAGAATTATGATCTTGAAGTTATAACTGTGATCTGAAATGTGT  
GGTGGTATGACAGCATAACATTAAACATTACATCACAGCTCAAAGGACTGTGATATAATCCATTATAC  
AACTCAAAGGACTGTGATATAATCCATTATACAGCTCACAGTTCTGAAAATGTATAAAAGAATCTATAAT  
CTAGTACTGAAATTACTAAATTGGTAAGATGATTAAATGATTAAATTAAACATTATCTAGAATATAT  
GGCTCCATTATTTATTTATAGTGTAAAGTTGTATTCTAAAGTTGTGTTGTGACAGTATCTTAAATGAG  
TCTTAAAAAATAAAGGCATATTGTTCATGTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAA

## FIGURE 43

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48296  
><subunit 1 of 1, 515 aa, 1 stop  
><MW: 56885, pi: 6.49, NX(S/T): 5  
MAPRGCAGHPPPSQACVCPGKMLAMGALAGFWILCLLTYGYLSWGQALEEEEGLAQA  
GEKLEPSTTSTSQPHLIFILADDQGFRDVGYHGSEIKPTLDKLAEGVKLENYYVQPICTP  
SRSQFITGKYQIHTGLQHSIIRPTQPNCPLDNATLPQKLKEVGYSTHMVGKWHLGFRKEC  
MPTRRGFDTFFGSLLGSGDYYTHYKCDSPGMCGYDLYENDNAAWDYDNGIYSTQMYTQRVQQ  
ILASHNPTKPIFLYTAYQAVHSPLQAPGRYFEHYRSIININRRYAAMLSCLDEAINVTIA  
LKTYGFYNNSIIYSSDNGGQPTAGGSNWPLRGSKGTWEGGIRAVGVHSPLLKNKGTVC  
ELVHITDWYPTLISLAEGQIDEEDIQLDGYDIWETISEGLRSPRVDILHNIDPYTPRQKMAPG  
QQAMGSGTLQSSQPSECSTGNCLQEILATATGSPLSLSATWDRTGGTMNGSPCQLAKVYGFS  
TSQPTHMRGWTYLTGIQES

**Important Features:**

**Signal Peptide:**

amino acids 1-37

**Sulfatases signature 1.**

amino acids 120-132

**Sulfatases signature 2.**

amino acids 168-177

**Tyrosine kinase phosphorylation site.**

amino acids 163-169

**N-glycosylation sites.**

amino acids 157-160, 306-309 and 318-321

## **FIGURE 44**

CGGACGCGTGGGTGCGAGTGGAGCGGAGGACCCGAGCGGCTGAGGGAGAGAGGGAGGCAGCAGGAC  
TTAGCTGCTACGGGGTCCGGCCGGCCCTCCGAGGGGGCTCAGGAGGAGGAAGGGAGGAC  
CCGTGCGAGAATGCCTCTGCCCTGGAGCCTGCGCTCCGCTGCTCTCCTGGTGGCAG  
GTGGTTCGGAACCGCGCAGTGCAAGGCATCACGGGTGTTAGCATCGGCACGTCAAGCCT  
GGGGTCTGTCACTATGGAACATAACTGGCTGCTGCTACGGCTGGAGAAGAAAACAGCAAGGG  
AGTCTGTGAAGCTACATGCGAACCTGGATGTAAGTTGGTAGTGCCTGGACCAAACAAAT  
GCAGATGCTTCCAGGATACACCGGAAACCTGCAGTCAGATGTAATGAGTGTGGAAATG  
AAACCCGGCCATGCCAACACAGATGTTGAATACACACCGAAGCTACAAGTGCTTGCCT  
CAGTGGCCACATGCTCATGCCAGATGCTACGTGTGAACTCTAGGACATGTGCCATGATAA  
ACTGTCAGTACAGCTGTGAAGACACAGAAGAAGGGCACAGTGCTGTGCTCATCCTCAGGA  
CTCCGCCTGGCCCCAATGGAAGAGACTGTCTAGATATTGATGAATGTGCCTCTGGTAAAGT  
CATCTGTCCTACAATCGAAGATGTTGAACACACATTGGAAGCTACTACTGCAAATGTCACA  
TTGGTTCGAACTGCAATATATCAGTGGACGATATGACTGTATAGATATAATGAATGACT  
ATGGATAGCCATACGTGCAGCCACCATGCCATTGCTCAATACCCAAGGGCTTCAAGTG  
TAAATGCAAGCAGGGATATAAGGCAATGGACTTCGGTGTCTGCTATCCCTGAAAATTCTG  
TGAAGGAAGTCCTCAGAGCACCTGGTACCATCAAAGACAGAATCAAGAAGTTGCTTGCTCAC  
AAAAACAGCATGAAAAAGAAGGCAAAATTAAAAATGTTACCCAGAACCCACCAGGACTCC  
TACCCCTAAGGTGAACTTGCAGCCCTCAACTATGAAGAGATAGTTCCAGAGGGCGGAAC  
CTCATGGAGGTAAAAAAGGAAATGAAGAGAAATGAAAGAGGGCTTGAGGATGAGAAAAGAG  
AAGAGAAAGCCCTGAAGAATGACATAGAGGAGCGAACGCTGCGAGGAGATGTGTTTCCCT  
AAGGTGAATGAAGCAGGTGAATTGGCCTGATTCTGGTCCAAAGGAAAGCGCTAACCTCAA  
ACTGGAACATAAAGATTAAATATCTGGTTGACTGCAGCTCAATCATGGGATCTGTGACT  
GGAAACAGGATAGAGAAGATGATTTGACTGGAATCCTGCTGATCGAGATAATGCTATTGGC  
TTCTATATGGCAGTTCCGGCCTTGGCAGGTACAAGAAAGACATTGGCGATTGAAACTTCT  
CCTACCTGACCTGCAACCCCAAAGCAACTTCTGTTGCTTTGATTACGGCTGGCCGGAG  
ACAAAGTCGGAAACTTCGAGTGTGAAAACAGTAACAATGCCCTGGCATGGGAGAAG  
ACCACGAGTGGAGGATGAAAAGTGGAGACAGGGAAAATTGAGTGTATCAAGGAACTGATGC  
TACCAAAAGCATCATTGGTAAAGCAGAACGTGCAAGGGAAAACCGGCAAATCGCAGTGG  
ATGGCGTCTGCTTGTGTTGAGGCTTATGTCAGATGCTTATCTGTGGATGACTGAATG  
TTACTATCTTATATTGACTTGTATGTCAGTCCCTGGTTTTGATATTGCATCATAG  
GACCTCTGGCATTAGAATTACTAGCTGAAAATTGTAATGTACCAACAGAAATATTATTG  
TAAGATGCCTTCTTGTATAAGATATGCCAATATTGCTTAAATATCATATCACTGTATCT  
TCTCAGTCATTCTGAATCTTCCNCATTATATTATAAAATNTGAAANGTCAGTTATCTC  
CCCTCCTCNGTATATCTGATTGTATANGTANGTTGATGNGCTCTCTACAACATTCTA  
GAAAATAGAAAAAAAGCACAGAGAAATGTTAAGTGTGACTCTTATGATAACTCTTGG  
AACTATGACATCAAAGATAGACTTTGCCTAAGTGGCTAGCTGGTCTTCATAGCCAAAC  
TTGTATATTAAATTCTTGTAAATAATAA

## **FIGURE 45**

MPLPWSLALPLLLSWVAGGFGNAAASARHHGLLASARQPGVCHYGTKLACCYGWRNSKGVCE  
ATCEPGCKFGECPGNKCRCPGTYGKTCSDVNECGMKPRPCQHRCVNTHGSYKCFCLSGH  
MLMPDATCVNSRTCAMINCQYSCEDTEEGPQCLCPSSGLRAPNGRDCLDIDECAKGKVICP  
YNRRCVNTFGSYYCKCHIGFELQYISGRYDCIDINECTMDSHTCSHHANCFTQGSFKCKCK  
QGYKGNGLRCSAIPENSVKEVLRAPGTIKDRIKKLLAHKNNSMKKAKIKNVTPEPTRTPPK  
VNLQPFNYEEIVSRGGNSHGGKGNEEK

**Signal peptide:**

amino acids 1-21

**EGF-like domain cysteine pattern signature.**

amino acids 80-91

**Calcium-binding EGF-like domains**

amino acids 103-124, 230-251 and 185-206

## **FIGURE 46**

GGGAGCTGCTGCTGTGGCTGCTGGTGTGCGCGCTGCTCCTGCTCTTGGTGCAGCTGCTG  
CGCTTCCTGAGGGCTGACGGCGACCTGACGCTACTATGGGCCAGTGGCAGGGACGACGCC  
AGAATGGGAGCTGACTGATATGGTGGTGTGGGTACTGGAGCCTCGAGTGGATTGGTGAGG  
AGCTGGCTTACCAGTTGTCTAAACTAGGAGTTCTCTTGCTGTCAAGCCAGAAGAGTCAT  
GAGCTGGAAAGGGTGAAGAAGATGCCTAGAGAATGCAATTAAAAGAAAAAGATATACT  
TGTGTTGCCCTTGACCTGACCGACACTGGTCCCCATGAAGCGGCTACCAAAGCTGTTCTCC  
AGGAGTTGGTAGAACATCGACATTCTGGTCAACAATGGTGAATGTCCCAGCGTTCTGTGC  
ATGGATACCAGCTGGATGTCTACAGAAAGCTAACAGAGCTTAACACTTAGGGACGGTGTG  
CTTGACAAAATGTGTTCTGCCTCACATGATCGAGAGGAAGCAAGGAAAGATTGTTACTGTGA  
ATAGCATCCTGGGTATCATATCTGTACCTCTTCCATTGGATACTGTGCTAGCAAGCATGCT  
CTCCGGGGTTTTTAATGGCCTCGAACAGAACATTGCCACATACCCAGGTATAATAGTT  
TAACATTTGCCAGGACCTGTGCAATCAAATATTGTGGAGAATTCCCTAGCTGGAGAAGTCA  
CAAAGACTATAGGCAATAATGGAGACCAGTCCCACAAGATGACAACCAGTCGTTGTGCGG  
CTGATGTTAACATCAGCATGGCCAATGATTGAAAGAAGTTGGATCTCAGAACACCTTCTT  
GTTAGTAACATATTGTGGCAATACATGCCAACCTGGGCTGGATAACCAACAAGATGG  
GGAAGAAAAGGATTGAGAACCTTAAGAGTGGTGTGGATGCAGACTCTCTTATTAAAATC  
TTAAGACAAAACATGACTGAAAAGAGCACCTGTACTTTCAAGCCACTGGAGGGAGAAATG  
GAAAACATGAAAACAGCAATCTCTTATGCTTCTGAATAATCAAAGACTAATTGTGATT  
ACTTTTAATAGATATGACTTGTGCTTCAACATGGAATGAAATAAAAATAATAAAAAG  
ATTGCCATGAATCTGCAAAA

## FIGURE 47

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA36343
><subunit 1 of 1, 289 aa, 1 stop
><MW: 32268, pI: 9.21, NX(S/T): 0
MVVWVTGASSGIGEELAYQLSKLGVSLVLSARRVHELERVKRRCLEGNLKEKDILVLPLDL
TDTGSHEAATKAVLQEFGRIDILVNNGGMSQRSLCMDTSLDVYRKLIELNYLGTVSLTKCVL
PHMIERKQGKIVTVNSILGIISVPLSIGYCASKHALRGFFNGLRTELATYPGIIVSNICPGP
VQSNIVENSLAGEVTKTIGNNGDQSHKMTTSRCVRLMLISMANDLKEVWIEQPFLLVTLW
QYMPTWAWWITNKGKKRIENFKSGVDADSSYFKIFKTKHD
```

**Important Features:**

**Signal Peptide:**

amino acids 1-31

**Transmembrane domain:**

amino acids 136-157

**Tyrosine kinase phosphorylation site.**

106-113 and 107-114

**Homologous region to Short-chain alcohol dehydrogenase**

amino acids 80-90, 131-168, 1-13 and 176-185

## FIGURE 48

GCGACGTGGGCACCGCCATCAGCTGTTCGCGCGTCTTCTCCTCCAGGTGGGGCAGGGGTTTC  
GGGCTGGTGGAGCATGTGCTGGGACAGGAACAGCATCCTCAATCAATCAAACAGCATATTGG  
TTGCATCTTCTACACACTACAGCTATTGTTAGGTTGCCTGCGGACACGCTGGGCCTGTCC  
**TGATG**CTGCTGAGCTCCCTGGTCTCTCGCTGGTCTGTCTACCTGGCCTGGATCTGTTC  
TTCGTGCTCTATGATTCTGCATTGTTGTATCACCACTATGCTATCAACGTGAGCCTGAT  
GTGGCTCAGTTCCGGAAGGTCCAAGAACCCCCAGGGCAAGGCTAAGAGGCAGTGAGCCCTCA  
ACCCAAGCCAGGCTGACCTCATCTGCTTGGCTTCAGCCGCTCAGCGTGCCTGT  
GACAGCGTGGCCCCGGCCCCCAAGCCTCAGGAGGGCAACACAGTCCCTGGCGAGTGGCCC  
TGGCAGGCCAGTGTGAGGAGGCAAGGAGCCCACATCTGCAGCGGCTCCCTGGTGGCAGACAC  
CTGGGTCCCTCACTGCTGCCACTGCTTGAAAAGGCAGCAGCAACAGAACTGAATTCTGGT  
CAGTGGTCCTGGGTTCTGAGCGTGAGGGACTCAGCCCTGGGCCAAGAGGTGGGGTG  
GCTGCCCTGCAGTTGCCAGGGCTATAACCACACTACAGCCAGGGCTCAGACCTGGCCCTGCT  
GCAGCTCGCCCACCCCCACGACCCACACACCCCTCTGCCTGCCAGCCGCCATCGCTTCC  
CCTTGGAGCCTCCTGCTGGCCACTGGCTGGGATCAGGACACCACTGATGCTCCTGGGACC  
CTACGCAATCTGCCTCGTCTCATCAGTGCCTCACAGTCAACTGTATCTACAACCAGCT  
GCACCAGCGACACCTGTCCAACCCGGCCGGCTGGGATGCTATGTGGGGCCCCAGCCTG  
GGGTGCAGGGCCCCCTGTCAAGGAGATTCCGGGGCCCTGTGCTGTGCCTGAGCCTGACGGA  
CACTGGGTTCAAGGCTGGCATCATCAGCTTGATCAAGCTGTGCCAGGAGGACGCTCCTGT  
GCTGCTGACCAACACAGCTGCTCACAGTTCTGGCTGCAGGCTCGAGTTCAAGGGGGCAGCTT  
TCCTGGCCCAGAGCCCAGAGACCCGGAGATGAGTGTGAGGACAGCTGTGTAGCCTGTGGA  
TCCTTGAGGACAGCAGGTCCCCAGGCAGGAGCACCCCTCCCCATGCCCTGGGAGGCAGGCT  
GATGCACCAAGGGACAGCTGGCTGTGGCGGAGCCCTGGTGTAGGAGGAGGCGGTGCTAAGT  
CTGCCCACTGCTTCATTGGCGCCAGGCCAGAGGAATGGAGCGTAGGGCTGGGACCAAGA  
CCGGAGGAGTGGGGCTGAAGCAGCTCATCCTGCATGGAGCCTACACCCACCCCTGAGGGGG  
CTACGACATGCCCTCCTGCTGGCCAGGCCCTGTGACACTGGAGGCCAGCCTGCCGGCCCC  
TCTGCCTGCCCTATCCTGACCAACACCCTGCCTGATGGGAGCGTGGCTGGTTCTGGGACGG  
GCCGCCAGGAGCAGGCATCAGCTCCCTCAGACAGTGCCTGACCCCTCTGGGGCTAG  
GCCCTGCAGCCGGCTGCATGCAGCTCTGGGGTGTGGCAGGCCATTCTGCCGGGGATGG  
TGTGTACCACTGCTGTGGGTGAGCTGCCAGCTGTGAGGGCTGTCTGGGGCACCACGGTG  
CATGAGGTGAGGGCACATGGTTCTGGCCGGCTGCACAGCTCGAGATGCTTGCCTAAGG  
CCCCGCCAGGCCGGCTTCACCGCGCTCCCTGCCTATGAGGACTGGGTCAAGCAGTTGG  
ACTGGCAGGTCTACTTCGCCAGGAACCAAGAGCCCGAGGCTGAGCCTGGAAGCTGCTGGCC  
AACATAAGCCAACCAACCAGCTGCT**TGA**CAGGGGACCTGCCATTCTCAGGACAAGAGAAATGC  
AGGCAGGCAAATGGCATTACTGCCCTGTCTCCCCACCCCTGTATGTGTGATTCCAGGCAC  
CAGGGCAGGCCAGAACGCCAGCAGCTGTGGGAAGGAACCTGCCTGGGCCACAGGTGCCCA  
CTCCCCACCCCTGCAGGACAGGGGTGTCTGTGGACACTCCCACACCCAACTCTGCTACCAAGC  
AGGCCTCAGCTTCTCCTCTTACTCTTCAGATAACATCACGCCAGCCACGTTGTT  
TGAAAATTCTTTGGGGGGCAGCAGTTCTTTAAACTTAAATAATTGTTAC  
AAAATAAAA

## **FIGURE 49**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA40571
MLLSSLVSLAGSVYLAWILFFVLYDFCIVCITYAINVSLMWLSFRKVQEPOGKAKRHGNTV
PGEWPWQASVRQGAHICSGSLVADTWVLTAAHCFEKAATELNSWSVVLGSLQREGLSPGA
EEVGVAALQLPRAYNHYSQGSDLALLQLAHPTTHTPLCLPQPAHRFPFGASCWATGWDQDTS
DAPGTLRNLRRLRISRPTCNCIYNQLHQRHLSNPAPGMLCGGPQPGVQGPCQGDGGPVLC
LEPDGHWVQAGIISFASSCAQEDAPVLLNTAAHSSWLQARVQGAFLAQSPETPEMSDEDS
CVACGSLRTAGPQAGAPSPWPWEARLMHQQLACGGALVSEEAVLAAHCFIGRQAPEEWSV
GLGTRPEEWGLKQLILHGAYTHPEGGYDMALLLAQPVTLGASLRPLCLPYPDHHLPDGERG
WVLGRARPAGISSLQTVPVTLLGPRACSRHLAAPGGDGSPILPGMVCTSAVGELPSCEGLS
GAPLVHEVRGTWFLAGLHSFGDACQGPAPAVFTALPAYEDWVSSLDWQVYFAEEPEPEAEP
GSCLANISQPTSC
```

**Important features:**

**Signal peptide:**

amino acids 1-15

**Homologous region to Serine proteases, trypsin family**

amino acids 79-95, 343-359 and 237-247

**N-glycosylation sites.**

amino acids 37-40 and 564-567

**Kringle domains**

amino acids 79-96, 343-360 and 235-247

## **FIGURE 50**

CGGGCCGCCCGCCCCATTGGGCCGGGCTCGCTGGCGGGCAGGGGCAGCCTCACGGAGCTGAGCCAGGGCTGGCATGGGTGT  
GCCGCGTCCCTGAGTCCCAGAGTCGGCGGGCGGGCAGGGGCAGCCTCACGGAGCTGAGCCAGGGCTGGCATGGGTGT  
CCCAGCTGTAGCCGCCTCACAGGAAGATGCTGCGTCGGCGGGCAGCCTGCACGGAGCTGAGGGTCCAGG  
GCATGTGGGTGCAGCCCTGGGAGCACTGTGGTTCTGCCTCACAGGAAGCCCTGGAGGTCCAGG  
TCCCTGAAGACCCAGTGGTGGCACTGGTGGCACCCGATGCCACCCCTGTGCTGCTCCTCTCC  
CCTGAGCCTGGCTCAGCCTGGCACAGCTAACCTCATCTGGCAGCTGACAGATAACAAACA  
GCTGGTGCACAGCTTGCTGAGGGCCAGGACCAGGGCAGCGCCTATGCCAACCGCACGGCCC  
TCTTCCGGACCTGCTGGCACAGGGCACCGATCCCTGAGGCTGCAGCGCGTGCAGGGCG  
GACGAGGGCAGCTTCACCTGCTGAGCATCCGGATTTCGGCAGCGCTGCCGTAGCCT  
GCAGGGTGGCCGCTCCCTACTCGAAGCCCAGCATGACCCCTGGAGGCCAACAAAGGACCTGCGGC  
CAGGGGACACGGTGACCATCACGTGCTCCAGCTACCAGGGCTACCCTGAGGCTGAGGTGTT  
TGGCAGGGATGGCAGGGTGTGCCCTGACTGGCACAGTGACCGTGCAGATGGCCAACGA  
GCAGGGCTTGTGATGTGCACAGCGTCCTGCGGGTGGTGTGGGTGCGAATGGCACCTACA  
GCTGCCTGGTGCACACCCGTGCTGCAGCAGGATGCGCACRGCTCTGTCACCATCACAGGG  
CAGCCTATGACATTCCCCCAGAGGCCCTGTGGGTGACCGTGGCTGTCTGTCTCAT  
TGCAC TGCTGGTGGCCCTGGCTTCTGTGCTGGAGAAAGATCAAACAGAGCTGTGAGGAGG  
AGAATGCAGGAGCTGAGGACCAGGATGGGAGGGAGAAGGCTCCAAGACAGCCTGCAGCCT  
CTGAAACACTCTGACAGCAAAGAAGATGATGGACAAGAAATAGCCTTGACCATGAGGACCAAGG  
GAGCTGCTACCCCTCCCTACAGCTCCTACCCCTGGCTGCAATGGGCTGCACGTGAGGCC  
TGCCCCAACAGATGCATCCTGCTCTGACAGGTGGCTCCTCTCAAAGGATGCGATAACAC  
AGACCACTGTGCAGCCTTATTCTCCAATGGACATGATTCCAAGTCATCCTGCTGCCTTT  
TTCTTATAGACACAATGAACAGACCACCAACCTTAGTTCTTAAGTCATCCTGCCTGCT  
GCCCTATTCACAGTACATACATTCTTAGGGACACAGTACACTGACCAATCACCACCTC  
TTCTTCCAGTGTGCGTGGACCATCTGGCTGCCTTTCTCCAAAAGATGCAATATTCAA  
CTGACTGACCCCTGCCTTATTCAACAAAGACACGATGCATAGTCACCCGGCTTGT  
TCCAATGGCGTGATAACTAGTGTGATCATGTTCAAGCCCTGCTTCCACCTGCATAGAATCTT  
TCTTCTCAGACAGGGACAGTGCAGGCTCAACATCTCCTGGAGTCTAGAAGCTGTTCT  
CCCTCCTCCTCCCTGCCCAAGTGAAGACAGGGCAGGGCAGGAATGCTTGGGACACCG  
AGGGGACTGCCCGCCCCACCCCCACCATGGTGTATTCTGGGCTGGGCAGTCTTCC  
TTGCCTCTGGCCAGCTCCTGGCCTCTGGTAGAGTGAGACTTCAGACGTTCTGATGCCTCCG  
GATGTGATCTCTCCCTGCCCAAGGAATGAAAGATGTGAGGACTTCTAATTAAATGT  
TCGGAGGGATTTGTAACACTGGGGTATATTGGGAAATAAATGTCTTGTAAAAAAA  
AAAAAAAAAAAAAA

## FIGURE 51

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA41386
><subunit 1 of 1, 316 aa, 1 stop, 1 unknown
><MW: -1, pI: 4.62, NX(S/T): 4
MLRRRGSPGMGVHVGAAALGALWFCLTGALEVQVPEDPVVALVGTATLCCSFSPFGFSLAQ
LNLIWQLTDTKQLVHSFAEGQDQGSAYANRTALFPDLLAQGNASLRLQRVRVADEGSFTCFV
SIRDFGSAAVSLQVAAPYSKPSMTLEPNKDLRPGDTVTITCSSYQGYPEAEVFWQDGQGVPL
TGNVTTSQMANEQGLFDVHSVLRVVLGANGTYSCLVRNPVLQQDAHXSVTITGQPMTFPPEA
LWVTVGLSVCLIALLVALAFVCWRKIKQSCEEENAGAEDQDGEGEGSKTALQPLKHSDSKED
DGQEIA
```

**Important features:**

**Signal peptide:**

amino acids 1-28

**Transmembrane domain:**

amino acids 251-270

**N-glycosylation site.**

amino acids 91-94, 104-107, 189-192 and 215-218

**Homologous region to Immunoglobulins and MHC**

amino acids 217-234

## **FIGURE 52**

TTCGTGACCCTTGAGAAAAGAGTTGGTGGTAATGTGCCACGTCTTCTAAGAAGGGGGAGTC  
CTGAACTTGTCTGAAGCCCTGTCCGTAAAGCCTTGAACCTACGTTCTTAAATCTATGAAGTCG  
AGGGACCTTCGCTGCTTTGTAGGGACTTCTTCCTGCTTCAGCAACATGAGGCTTTCT  
TGTGGAACCGCGTCTTGACTCTGTCGTCACTCTTGTATTGGGGCTTGATCCCTGAACCA  
GAAGTAAAATTGAAGTTCTCCAGAACGCATTCTGCCATCGCAAGACCAAAGGAGGGGA  
TTTGATGTTGGTCCACTATGAAGGCTACTTAGAAAAGGACGGCTCCTTATTTCACTCCACTC  
ACAAACATAACAATGGTCAGCCCATTGGTTACCTGGCATCTGGAGGCTCTCAAAGGT  
TGGGACCAGGGCTTGAAGGAATGTGTAGGAGAGAAGAGAAAGCTCATCATTCCCTGC  
TCTGGGCTATGGAAAAGAAGGAAAAGTAAAATTCCCCAGAAAGTACACTGATATTAAATA  
TTGATCTCCTGGAGATTCGAAATGGACCAAGATCCCAGAATCATTCCAAGAAATGGATCTT  
AATGATGACTGGAAACTCTCTAAAGATGAGGTAAAGCATATTAAAGAAGGAGTTGAAAAA  
ACATGGTGCCTGGTGAATGAAAGTCATCATGATGCTTGGTGGAGGATATTTTGATAAAG  
AAGATGAAGACAAAGATGGGTTATATCTGCCAGAGAATTACATATAAACACGATGAGTTA  
**TAGAGATACATCTACCCCTTTAATATAGCACTCATCTTCAAGAGAGGGCAGTCATCTTAA**  
AGAACATTTATTTTATACAATGTTCTTCTGCTTGTGTTTATTTTATATATTTTT  
CTGACTCCTATTTAAAGAACCCCTTAGGTTCTAAGTACCCATTCTTCTGATAAGTTATT  
GGGAAGAAAAGCTAATTGGCTTTGAATAGAAGACTTCTGGACAATTTTCACTTCACAG  
ATATGAAGCTTGTGTTACTTCACTTATAAATTAAAATGTTGCAACTGGGAATATACC  
ACGACATGAGACCAGGTTATAGCACAAATTAGCACCCCTATATTCTGCTTCCCTTATTTTC  
TCCAAGTTAGAGGTCAACATTGAAAAGCCTTTGCAATAGCCCAAGGCTTGCTATTTCAT  
GTTATAATGAAATAGTTATGTGTAACTGGCTCTGAGTCTGCTTGAGGACCAGAGGAAAA  
TGGTTGTTGGACCTGACTTGTAAATGGCTACTGCTTACTAAGGAGATGCAATGCTGAAG  
TTAGAAACAAGGTTAATAGCCAGGCATGGTGGCTCATGCCTGTAATCCCAGCACTTGGGAG  
GCTGAGGCGGGCGGATCACCTGAGGTTGGAGTCGAGACCAGCCTGACCAACACGGAGAAA  
CCCTATCTACTAAAATACAAAGTAGCCCAGCGTGGTATGCGTGCCTGTAATCCCAGCT  
ACCCAGGAAGGCTGAGGCGGCAGAACATCAATTGAAACCCGAGGCCAGGTTGCGGTAAGCCGAG  
ATCACCTNCAGCCTGGACACTCTGCTCGAAAAAAAGAAAAGAACACGGTTAATACCATATNA  
ATATGTATGCATTGAGACATGCTACCTAGGACTTAAGCTGATGAAAGCTTGGCTCCTAGTGT  
TGGTGGCTATTATGATAAAATAGGACAAATCATTATGTGTGAGTTCTTGTAAATAAAATG  
TATCAATATGTTAGATGAGGTAGAAAGTTATTTATATTCAATATTACTTCTTAAGGC  
TAGCGGAATATCCTTCTGGTTCTTAAATGGGTAGTCTAGTATATTACTACAATAACA  
TTGTATCATAAGATAAAAGTAGTAAACCAGTCTACATTCCCATTCTGCTCATAAAAAC  
TGAAGTTAGCTGGGTGTGGCTCATGCCTGTAATCCCAGCACTTGGGGCCAAGGAGGG  
TGGATCACTTGAGATCAGGAGTTCAAGACCAAGCAGCCTGGCCAACATGGTGAACCTTGTCTCTA  
CTAAAAATACAAAATTAGCCAGGCGTGGTGGTCACACCTGAGTCCCAGCTACTCGGGAG  
GCTGAGACAGGAGATTGCTTGAACCCGGAGGCAGGTTGCAAGTCAAGGAGATTGTGCC  
ACTGCACTCCAGCCTGGGTGACAGAGCAAGACTCCATCTAAAAAAAAAGAAGCAGA  
CCTACAGCAGCTACTATTGAATAAACCTATCCTGGATTTT

## FIGURE 53

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44194
><subunit 1 of 1, 211 aa, 1 stop
><MW: 24172, pI: 5.99, NX(S/T): 1
MRLFLWNAVLTLFVTSLIGALIPEPEVKIEVLQKPFICHRKTGGDLMLVHYEGYLEKD GSL
FHSTHKHNNNGQPIWFTLGLILEALKGWDQGLKGMCVGEKRKLIIPPALGYGKEGKGKIPPEST
LIFNIDLLEIRNGPRSHESFQEMDLNDDWKLSKDEVKAYLKKEFEKHGAVVNESHHDALVED
IFDKEDEDKDGFISAREFTYKHDEL
```

**Important features:**

**Signal peptide:**

amino acids 1-20

**N-glycosylation site.**

amino acids 176-179

**Casein kinase II phosphorylation site.**

amino acids 143-146, 156-159, 178-181 and 200-203

**Endoplasmic reticulum targeting sequence.**

amino acids 208-211

**FKBP-type peptidyl-prolyl cis-trans isomerase**

amino acids 78-114 and 118-131

**EF-hand calcium-binding domain.**

amino acids 191-203, 184-203 and 140-159

**S-100/ICaBP type calcium binding domain**

amino acids 183-203

## **FIGURE 54**

AATAAAGCTCCTTAATGTTGATATGTCCTTGAAGTACATCCGTGCATTTTTTAGCAT  
CCAACCATTCCCTCCCTTGAGTTCTGCCCTCAAATCACCTCTCCGTAGCCCACCGA  
CTAACATCTCAGTCTGAAA**ATG**CACAGAGATGCCTGGCTACCTCGCCCTGCCTCAGCCT  
CACGGGGCTCAGTCTTTCTCTTGGTGCCACCAGGACGGAGCATGGAGGTACAGTAC  
CTGCCACCCCTCAACGTCTCAATGGCTCTGACGCCGCTGCCCTGCACCTCAACTCCTGC  
TACACAGTGAACCACAAACAGTTCTCCCTGAACCTGGACTTACCAAGGAGTGAACAACACTGCTC  
TGAGGAGATGTTCTCCAGTTCAGCATGAAGATCATTAAACCTGAAGCTGGAGCGGTTCAAG  
ACCGCGTGGAGTTCTCAGGGAACCCCAGCAAGTACGATGTGTCGGTATGCTGAGAACGTG  
CAGCCGGAGGATGAGGGATTACAACGTCTACATCATGAACCCCCCTGACCGCCACCGTGG  
CCATGGCAAGATCCATCTGCAGGTCTCATGGAAGAGCCCCCTGAGCGGGACTCCACGGTGG  
CCGTGATTGTGGGTGCCCTCCGTCGGGGCTTCTGGCTGGTCATCTTGGTGCATGGTG  
GTCAAGTGTGTGAGGAGAAAAAAAGAGCAGAACCGGATGATGGCGCAAG**TAG**TGGTGGCGGCC  
CTGCAGCCTCCGTCTCCGTCTCCCTCTCCGCTGTACAGTACCTGCCTGCTCG  
CTCTTGGTGTGCTTCCCGTACCTAGGACCCCAGGGCCACCTGGGGCCTCCTGAACCCCCG  
ACTTCGTATCTCCACCCCTGCACCAAGAGTGACCCACTCTTCCATCGAGAACCTGCCA  
TGCTCTGGACGTGTGGGCCCTGGGAGAGGAGAGAAAGGGCTCCACCTGCCAGTCCCTGG  
GGGGAGGCAGGAGGCACATGTGAGGGCCCCAGAGAGAACGGAGTGGTGGCAGGGTAGA  
GGAGGGCCGCTGTCACCTGCCAGTGCTTGCCTGGCAGTGGCTTCAGAGAGGACCTGGTGG  
GGAGGGAGGGCTTCCTGTGCTGACAGCGCTCCCTCAGGAGGGCCTGGCCTGGCACGGCTG  
TGCTCCTCCCTGCTCCAGGCCAGAGCAGCCATCAGGCTGGAGGTGACGATGAGTCCCTGA  
AACTTGGAGGGCATGTTAAAGGGATGACTGTGCAATTCCAGGGACTGACGGAAAGCCAGGG  
CTGCAGGCAAAGCTGGACATGTGCCCTGGCCAGGAGGCCATGTTGGGCCCTCGTTCCATT  
GCTAGTGGCCTCCTGGGCTCCTGTTGGCTCTTAATCCCTTAGGACTGTGGATGAGGCCAG  
ACTGGAAGAGCAGCTCCAGGTAGGGGCCATGTTCCAGCGGGGACCCACCAACAGAGGCC  
AGTTCAAAGTCAGCTGAGGGCTGAGGGGTGGGCTCCATGGTGAATGCAGGTTGCTGCAG  
GCTCTGCCTCTCCATGGGTAACCACCCCTGCCCTGGCAGGGCAGCCAAGGCTGGAAAT  
GAGGAGGCCATGCACAGGTGGGAGCTTCTTGGCTTCAAGAGAGGAAAGCCTGAGGCC  
GCCCTGGTGGGTTCCACCTGGCTTGGCTACAGAGAGGAAAGGAAAGCCTGAGGCC  
GCATAAGGGAGGCCTTGGAACCTGAGCTGCCAATGCCAGCCCTGCCCCATCTGCCAG  
CTACTCGCTCCTCTCCAAACAACCTCCCTCGTGGGACAAAAGTGACAATTGTAGGCCAGGC  
ACAGTGGCTCACGCCGTAAATCCCAGCAGCTTGGAGGCCAAGGGGGTGGATTACCTCCAT  
CTGTTAGTAGAAATGGGCAAACCCATCTCTACTAAAAAATACAAGAATTAGCTGGCGTG  
GTGGCGTGTGCTGTAATCCCAGCTATTGGGAGGCTGAGGAGGAGAATCGCTTGAGGCC  
GGAAGCAGAGGTTGCACTGAACTGAGATAGTGATAGTGCCACTGCAATTGCCAG  
ATAGAGAGACTCCATCTCAAAAAAA

## **FIGURE 55**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45415
<subunit 1 of 1, 215 aa, 1 stop
<MW: 24326, pI: 6.32, NX(S/T): 4
MHRDAWLPRPAFSLTGLSLFFSLVPPGRSMEVTVPATLNVLNGSDARLPCTFNSCYTVNHKQ
FSLNWTYQECNNCSEEMFLQFRMKIINLKLERFQDRVEFGNPSKYDVSVMLRNVQPEDEGI
YNCYIMNPDRHRGHGKIHQLQVLMEPPERDSTVAVIVGASVGGFLAVVILVLMVVKCVRRK
KEQKLSTDDLKTEEGKTDGEGNPDDGAK
```

**Important features:**

**Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 161-179

**Immunoglobulin-like fold:**

amino acids 83-127

**N-glycosylation sites.**

amino acids 42-45, 66-69 and 74-77

## **FIGURE 56**

GTTGTATATGTCCTGAAGTACATCCGTGCATTTTTAGCATCCAACCATCCTCCCTTGTA  
GTTCTCGCCCCCTCAAATCACCTCTCCCTAGCCCACCCNACTAACATCTCAGTCTTGAA  
AATGCACAGAGATGCCTGGCTACCTCGCCCTGCCTCAGCCTCACGGGCTCAGTCTCTTT  
TCTCTTGGTGCACCAGGACGGAGCATGGAGGTCCACAGTACCTGNCCACCCCTAACGTCC  
TCAATGGCTCTGACGCCCGCCTGCCCTTCAACTCCTGCTACACAGTGAACCACAAAC  
AGTTCTCCCTGAACTGGACTTACCAAGGAGTGCAACAAC TGCTCTGAGGAGATGTTCCCTCAG  
TTCCGCATGAAGATCATTAACCTGAAGCTGGAGCGGTTCAAGACCGCGTGGAGTTCTCAGG  
GAACCCCAGCAAGTACGATGTGTCGGTATGCTGAGAACGTGCAGCCGGAGGATGAGGGGA  
TTTACAAC TGCTACATCATGAACCCCCC

## **FIGURE 57**

TCACGGGGCTCATCTTTCTCTTGCTGCCACCAGGACGGAGCATGGAGGTNCACATA  
CCTGCCACCCCTAACGTCTCAATGGCTTGACGCCCGCCTGCCCTGCACCTCAACTCCNG  
CTACACAGTGAACCACAAACAGTTCTCCCTGAACCTGGATTACCAAGGAGTGCAACAACGGC  
TCTGAGGAGATGTTCCCTCCAGTTCCCGATGGAAGATCATTAAACCTGAAAGCTGGAAGCGG  
TTTCAAGAACCGCGTGGAAAGTTCTCAGGGAACCCCAGCAAGTACGATGTGTCGGTGATGC  
TGAGAACGTGCAGCCGGAGGATGAGGGGATTACAAC TGCTACATCATGAACCCCCC

## FIGURE 58

TGCGGCAGCGTCGTACACCATGGGCCTCCACCTCCGCCCTACCGTGTGGGCTGCTCCGGATGGCCTCTGT  
TCCCTTGCTGCTGCTAATGCTGCTCGCGGACCCAGCGCTCCGCCGGACGTCAACCCCCAGTGGTGTGGTCC  
CTGGTATTTGGTAACCAACTGGAAGCCAAGCTGGACAAGCCGACAGTGGTGCACACTACCTCTGCTCCAAGAAGA  
CCGAAAGCTACTTCACAACTGGCTGAACCTGGAACGTGTGCTGCCGTGATCATTGACTGCTGGATTGACAATA  
TCAGGCTGGTTACAACAAAACATCCAGGGCACCCAGTTCTGTATGGTGTGGATGTACGTGTCCCTGGCTTTG  
GGAAGACCTTCACTGGAGTTCTGGACCCCAGCAAAAGCAGCGTGGGTTCCATTTCCACACCAGGGTGGAGA  
GCCTTGTGGGTGGGCTACACACGGGTGAGGATGTCCGAGGGCTCCCTATGACTGGCCCGAGCCCCAAATG  
AAAACGGGCCACTTCTGGCCCTCCCGAGATGATCGAGGAGATGTACAGCTGTATGGGGGCCCGTGGTGC  
TGGTGGCCACAGTATGGCAACATGTACACGGCTCTACTTCTGCAAGCGGCAGGCCAGGGCTGGAAGGACAAGT  
ATATCCGGGCTTCGTGCACTGGGTGCGCCCTGGGGGGCGTGGCCAAGACCTGCGCTCTGGCTTCAGGAG  
ACAACAACCGATCCCAGTCATCGGCCCCCTGAAGATCCGGAGCAGCAGCGGTCACTGTCTCCACAGCTGGC  
TGCTGCCCTACAACATACATGGTACCTGAGAAGGTGTTGTCAGACACCCACAATCAACTACACACTGCGGG  
ACTACCGCAAGTTCTCAGGACATCGGCTTGAAGATGGCTGCTCATGCGGCAGGACACAGAAGGGCTGGTGG  
AAGCCACGATGCCACCTGGCGTGCAGCTGACTGCCTCTATGGTACTGGCTCCCACACCAGACTCCTTCTACT  
ATGAGAGCTCCCTGACCGTGAACCTAAAATCTGCTTGTGACGGCGATGGTACTGTGAACCTGAAGAGTGC  
TGCAGTGCCAGGGCTGGCAGAGCCGCAGGAGCACCAAGTGTGCTGCAGGAGCTGCCAGGCAGCAGCACATCG  
AGATGCTGGCAACGCCACCACCTGGCTATCTGAAACGTGCTCTGGGCTTGAAGGACACTGGCTTGTG  
CTCTGTGGCTGGCCGTGGACCTGCTGTTGCCCTCTGGGCTGTCATGCCACCGCCTGGGCTTGAAGGATTTGTGA  
CTCACCAATTCAAGGCCCGAGTCTTGGACTGTGAAAGCATCTGCCATGGGAAGTGCTTGTATCCTTCTCT  
GTGGCAGTGAAGAAGGAAGAAATGAGAGTCTAGACTCAAGGGACACTGGATGCCAGAATGCTGCTGATGGTGA  
ACTGCTGTGACCTTAGGACTGGCTTCAAGGGTGGACTGGCTGGCCCTGGTCCAGTCCCTGCTGGGCT  
TGTCCCCCTATTCTGTGGCTTTCATACTTGCCTACTGGCCCTGGCCCCGAGCCTTCTATGAGGGATGTT  
ACTGGCTGTGGTCTGTACCCAGGGTCCAGGGATCGGCTCTGGCCCTGGGTGACCTTCCACACACCA  
GCCACAGATAGGCCCTGCACACTGGTACGGTAGCTAGAGCTGCTGCCCTGGTGGCTTAGCTGGTGGCCAGCC  
TGACTGGCTTCTGGCGAGCCTAGTACTGCTGCCAGGGCAGTTGTTGCTGCTGGTCTCG  
CCTGGACATCTCACTCCACTCTAACCTCCCTACCCAGGAGCATTCAAGCTCTGGATGGCAGAGATGTG  
CCCCCAGTCCCGCAGGCTGTGTTCCAGGGCCCTGATTCTCGGATGTGCTATTGGCCCCAGGACTGAAGCTGC  
CTCCCTTCACCCCTGGGACTGTGGTCCAAGGATGAGAGCAGGGGTTGGAGCCATGCCCTCTGGGAACCTATGGA  
GAAAGGAATCAAGGAAGCAGCCAAGGCTGCTCGCAGCTCCCTGAGCTGCACCTTGTAAACCCACCATCA  
CACTGCCACCCCTGCCCTAGGGTCTACTAGTACCAAGTGGTCAGCACAGGGCTGAGGATGGGCTCTATCCAC  
CCTGGCCAGCACCCAGCTAGTGTGGACTAGCCCAGAAACTTGAATGGGACCTGAGAGAGCCAGGGTCCCC  
TGAGGGCCCCCTAGGGCTTCTGTCTGCCCTAGGGTGTCCATGGATCTCCCTGTGGCAGCAGGATGGAGAGT  
CAGGGCTGCCCTCATGGCAGTAGGCTAAGTGGGTGACTGGCCACAGGCCAGAAAAGGGTACAGCTCTAGGT  
GGGGTTCCCAAAGACGCCTTCAGGCTGGACTGAGCTGCTCTCCACAGGGTTCTGTGCAGCTGGATTTCCTCTG  
TTGCATACATGCCCTGGCATCTGTCTCCCCTTGTGAGTGGCCCCACATGGGCTCTGAGCAGGCTGTATCTG  
GATTCTGGCAATAAAAGTACTCTGGATGCTGAAAAAAAAAAAAAA

## **FIGURE 59**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44189  
><subunit 1 of 1, 412 aa, 1 stop  
><MW: 46658, pI: 6.65, NX(S/T) : 4  
MGLHLRPYRVGLLPDGLLFLLLLMLLADPALPAGRHPPVVLVPGDLGNQLEAKLDKPTVVH  
YLCSKKTESYFTIWLNLLELLPVIIDCWIDNIRLVYNKTSRATQFPDGVDVRVPGFGKTFSL  
EFLDPSKSSVGSYFHTMVESLVGWGYTRGEDVRGAPYDWRRAPNENGPYFLALREMIEEMYQ  
LYGGPVVLVAHSMGNMYTLYFLQRQPQAWKDKYIRAFVSLGAPWGGVAKTLRVLASGDNNRI  
PVIGPLKIREQQRSAVSTSLLPYNTWSPEKVFVQTPTINYTLRDYRKFFQDIGFEDGWLM  
RQDTEGLVEATMPPGVQLHCLYGTGVPTPDSFYYESFPDRDPKICFGDGDGTVNLKSALQCQ  
AWQSRQEHQVLLQELPGSEHIEMLANATTLAYLKRVLLGP

**Important features:**

**Signal peptide:**

amino acids 1-28

**Potential lipid substrate binding site:**

amino acids 147-164

**N-glycosylation sites.**

amino acids 99-102, 273-276, 289-292 and 398-401

**Lipases, serine proteins**

amino acids 189-201

**Beta-transducin family Trp-Asp repeat**

amino acids 353-365

## FIGURE 60

CGGACGCGTGGCGGACGCGTGGGCAGCAGCGGGCGGCGACGGCGACATGGAGAGCGGG  
GCCTACGGCGCGCCAAGGCAGGGCGGCTCCTCGACCTGCAGCGCTTCCTGACGCAGCCGCA  
GGTGGTGGCGCGCGCCGTGTGCTTGGTCTTCGCTTGATCGTGTCTCCTGCATCTATGGTG  
AGGGCTACAGCAATGCCAACGAGTCTAAGCAGATGTACTGCGTGTCAACCGAACGAGGAT  
GCCTGCCGCTATGGCAGTGCCATCGGGGTGCTGGCCTTCCTGGCCTCGGCCTTCTTGGT  
GGTCGACGCGTATTCCCCCAGATCAGCAACGCCACTGACCGCAAGTACCTGGTCATTGGTG  
ACCTGCTCTCTCAGCTCTGGACCTTCCTGTGGTTGGTTCTGCTTCCTCACCAAC  
CAGTGGGCAGTCACCAACCCGAAGGACGTGCTGGTGGGGCGACTCTGTGAGGGCAGCCAT  
CACCTTCAGCTTCTTCCATCTCCTGGGGTGTGCTGGCCTCCCTGGCCTACCAGCGCT  
ACAAGGCTGGCGTGGACGACTTCATCCAGAATTACGTTGACCCCACCCGGACCCAAACACT  
GCCTACGCCTCCTACCCAGGTGCATCTGTGGACAACCTACCAACAGCCACCCCTCACCAAGAA  
CGGGGAGACCACCGAGGGCTACAGCCGCCCCCTGTGTACTGAGTGGCGGTTAGCGTGGAA  
GGGGGACAGAGAGGGCCCTCCCTCTGCCCTGGACTTCCATCAGCCTCTGGAACTGCCA  
GCCCTCTCTTCACCTGTTCCATCCTGTGCAGCTGACACACAGCTAAGGAGCCTCATAGCC  
TGGCGGGGGCTGGCAGGCCACACCCCAAGTGCCTGTGCCAGAGGGCTCAGTCAGCCGCT  
CACTCCTCCAGGGCACTTTAGGAAAGGGTTTAGCTAGTGTCTCGCTTTAATGA  
CCTCAGCCCCGCCTGCAGTGGCTAGAACGCCAGCAGGTGCCATGTGCTACTGACAAGTGCCT  
CAGCTTCCCCCGGCCGGTCAGGCCGTGGAGCCGCTATTATCGCTCTGCCAAAG  
ACTCGTGGGGGCCATCACACCTGCCCTGTGCAGCGGAGCCGGACCAGGCTTGTGCTCCTCA  
CTCAGGTTGCTCCCTGTGCCACTGCTGTATGATCTGGGGGCCACCACCCCTGTGCCGGT  
GGCCTCTGGGCTGCCCTCCGTGGTGTGAGGGCGGGCTGGTGTCTAGGCACCTCCCTTG  
CTCCCACCCCTGGCAGCAGGGAAAGGGCTTGCCGTACAACACCCAGCTTATGTAATATT  
TGCAGTTGTTACTTAGGAAGCCTGGGAGGGCAGGGTCCCCATGGCTCCAGACTCTGTC  
TGTGCCGAGTGTATTATAAAATCGTGGGGAGATGCCGGCTGGATGCTGTTGGAGACG  
GAATAAATGTTCTCATTCAAAG

## **FIGURE 61**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48304
<subunit 1 of 1, 224 aa, 1 stop
<MW: 24810, pI: 4.75, NX(S/T): 1
MESGAYGAAKAGGSFDLRRFLTQPQVVARAVCLVFALIVFSCIYGEGLSNAHESKQMYCVFN
RNEDACRYGSAIGVLAFLASAFFLVVDAYFPQISNATDRKYLVIDLLFSALWTFLWFVGFC
FLTNQWAVTNPKDVLVGADSVRAAITFSFFSIFSWGVLASLAYQRYKAGVDDFIQNYVDPTP
DPNTAYASYPGASVDNYQQPPFTQNAETTEGYQPPPVY
```

**Important features:**

**Type II Transmembrane domain:**

amino acids 1-45

**Other transmembrane domains:**

amino acids 74-90, 108-126 and 145-161

**N-glycosylation site.**

amino acids 97-100

## **FIGURE 62**

GAGCCACCTACCCTGCTCCGAGGCCAGGCCTGCAGGGCTCATCGGCCAGGGTGTCACTGAGCAGAAGG**ATG**  
CCCGTGGCCGAGGCCCCAGGTGGCTGGCGGGCAGGGGACGGAGGTGATGGGAGGAAGCGGAGCCAGAGGGG  
ATGTTCAAGGCCTGTGAGGACTCCAAGAGAAAAGCCGGGCTACCTCCGCCTGGTGCCTCTGTTGTGCTGCTG  
GCCCTGCTCGTGCCTGGCTCGCGGGGGTGCTACTCTGGTATTCTTAGGGTACAAGGCGGAGGTGATGGTCAGC  
CAGGTGACTCAGGCAGTCTGCGTGTACTCAATGCCACTTCTCCAGGATCTTACCCGCCGGAACTAGTGCCT  
TTCCGCAGTCAAACGCCAAAGCCCAGAAGATGCTCAAGGAGCTCATCACAGCACCCGCCGGAACTTACTAC  
AACTCCAGCTCCGTCTATTCCCTTGGGGAGGGACCCCTCACCTGCTCTCTGGTCAATTCTCAAATCCCCGAG  
CACCGCCGGCTGATGCTGAGCCCCGAGGTGGTGCAGGCACTGCTGGTGGAGGAGCTGCTGTCACAGTCAACAGC  
TCGGCTGCCGTCCCCTACAGGGCCAGTACGAAGTGGACCCCGAGGCCTAGTGTATGCCAGGAGCCAGTGTGAAA  
GACATAGCTGATTGAATTCCACGCTGGGTTGTTACCGCTACAGCTACGTGGGCAGGGCCAGGTCTCCGGCTG  
AAGGGCCTGACCACCTGGCCTCCAGCTGCCTGTGGCACCTGCAGGGCCCAAGGACCTCATGCTCAAACCTCCGG  
CTGGAGTGGACGCTGGCAGAGTGGCCGGACCGACTGGCATGTATGACGTGGCCGGGCCCTGGAGAACAGGCTC  
ATCACCTGGTGTACGGCTGCAGGCCAGGAGCCCGTGGAGGTCTGGCGTCGGGGCCATCATGGCGGTC  
GTCTGGAAGAAGGCCCTGCAAGCTACTACGACCCCTTCGTGCTCTCGTGCAGCCGGTGGCTTCCAGGCCTGT  
GAAGTGAACCTGACGCTGGACAACAGGCTGACTCCAGGGCTCCTCAGCACCCCGTACTTCCCAAGCTACTAC  
TCGCCCCAAACCCACTGCTCCTGGCACCTCACGGTGCCTCTCTGGACTACGGCTTGGCCCTCTGGTTGATGCC  
TATGCACTGAGGAGGGAGAAGTATGATTGCGCTGCACCCAGGGCAGTGGACGATCCAGAACAGGAGGCTGTG  
GGCTGCGCATCTGCAGCCCTACGCCAGAGGATCCCGTGGTGGCCACGGCCGGGATCACCATCAACTTCACC  
TCCAGATCTCCCTCACCGGGCCGGTGTGCGGGTGCACTATGGCTGTACAAACCAGTCGGACCCCTGCCCTGG  
GAGTTCTCTGTTCTGTGAATGGACTCTGTGCTCTGCTGTGATGGGTCAAGGACTGCCCAACGGCCTGGAT  
GAGAGAAACTGCGTTGCAAGGCCACATTCACTGCAAAAGAGGACAGCACATGCATCTCACTGCCAAGGTCTGT  
GATGGCAGCCTGATTGCTCAACGGCAGCGATGAAGAGCAGTGCAGGAAGGGTGCCATGTGGACATTCA  
TTCCAGTGTGAGGACCGGAGCTGCGTAAGAACCCGAGTGTGATGGCGGCCAGTCAGGGACGGC  
TCGGATGAGGAGGACTGTGACTGTGGCCTCCAGGGCCCTCCAGGGCATTGTTGGTGGAGCTGTGCTCCGAG  
GGTAGTGGCCATGGCAGGCCAGCCTCCAGGTGCGACACATCTGTGGGGGGGCCCTCATGCTGACCGC  
TGGGTGATAACAGCTGCCACTGCTCCAGGAGGACAGCATGGCTCCACGGTGTGTTGGACCGTGTCCGG  
AAGGTGTCAGAACTCGCGCTGGCCTGGAGAGGTGTCCTCAAGGTGAGGCCCTGCTCTGCACCCGTACCA  
GAAGAGGACAGCCATGACTACGACGTGGCGCTGCTGCAGCTCGACCACCCGGTGGTGCCTGGCCGCGTGC  
CCCGTCTGCCTGCCCGCGCTCCACTTCTCGAGGCCGCTGCACTGCTGGATTACGGCTGGGGCGCCTTG  
CGCGAGGGCGGCCCATCAGCAACGCTCTGCAGAAAGTGGATGTCAGTTGATCCACAGGACCTGTGCAGCGAG  
GCCTATCGCTACCAGGTGACGCCAGCATGCTGTGCGCTACCGCAAGGGCAAGAAGGATGCCTGTCAGGGT  
GACTCAGGTGGTCCGCTGGTGTGCAAGGCACTCAGTGGCGCTGGTCTGGCGGGCTGGTCAAGACGTCCCC  
GGCTGTGGCCGGCTAACTACTTGGCGTCTACACCCGCATCACAGGTGTGATCAGCTGGATCCAGCAAGTGGT  
ACCT**GA**GGAAACTGCCCTGCAAAGCAGGGCCACCTCTGGACTCAGAGAGGCCAGGGCAACTGCCAAGCAGG  
GGGACAAGTATTCTGGCGGGGGTGGGGAGAGAGCAGGCCCTGTGGTGGCAGGGAGGTGGCATCTTGCTCGTCC  
CTGATGTCGCTCCAGTGATGGCAGGAGGATGGAGAAGTGCAGCAGCTGGGGGCTGGTCAAGACGTCCCC  
CAGGCCACACCCAGCCCTCTGCCTCCAAATTCTCTCTCCGCTCCCTCCACTGCTGCCATAATGCAAG  
GCAGTGGCTCAGCAGCAAGAATGCTGGTCTACATCCCGAGGAGTGTCTGAGGTGGCCCAACTCTGTACAGAGG  
CTGTTGGGAGGCTTGCCTCCAGAGAGCAGATTCCAGCTGGAGGCCCTGGTCAACTTGGGATCTGGGAAAT  
GGAAGGTGCTCCATCGGAGGGACCCCTAGAGCCCTGGAGACTGCGAGGTGGCCTGCTGCCACTGTAAGCAA  
AAGGTGGGGAGTCCCTGACTCCAGGGTCCCTGGCCACCCCTGCCCTGGAGGCCCTCACAGCCCAGACCC  
CACTGGGAGGTGAGCTCAGCTGCCCTTGGATAAAGCTGCTGATaaaaaaaaaaaaaaaaaaaaaaa

## **FIGURE 63**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49152
><subunit 1 of 1, 802 aa, 1 stop
><MW: 88846, pI: 6.41, NX(S/T): 7
MPVAEAPQVAGGQGDGGDGEAEPEGMFKACEDSKRKARGYLRLVPLFVLLALLVLASAGVL
LWYFLGYKAEVMVSQVYSGSLRVLNRHFSQDLTRRESSAFRSETAKAQKMLKELITSTRLGT
YYNSSSVYSFGEGLTCFFWFILQIPEHRRMLSPPEVVQALLVEELLSTVNSSAAVPYRAEY
EVDPEGLVILEASVKDIAALNSTLGCYRSYVGQGVRLKGPDHLASSCLWHLQGPKDML
KLRLLEWTLAECRDRLLAMYDVAGPLEKRLITSVYGCSRQEPPVVEVLAGAIMAVVWKGLHSY
YDPFVLSVQPVVFQACEVNLTLDNRLDSQGVLSTPYFPSPYSPQTHCSWHLTVPSLDYGLAL
WFDAYALRRQKYDLPCTQGQWTIQNRRLCGLRILQPYAERIPVVAATAGITINFTSQISLTGP
GVRVHYGLYNQSDPCPGEFLCSVNGLCVPACDGVKDCPNGLDERNCVCRATFQCKEDSTCIS
LPKVCDGQPDCNLNGSDEEQCQEGVPCGTFTQCEDRSCVKKPNPQCDGRPDCRDGSDEEHCD
CGLQGPSSRIVGGAVSSEGEWPWQASLQVGRGRHICGGALIADRWTAAHCFQEDSMASTVL
WTVFLGKVWQNSRWPGEVSKVSRLLLHPYHEEDSHDYDVALLQLDHPVVRSAAVRPVCLPA
RSHFFEPGLHCWITGWGALREGGPISNALQKVDVQLIPQDLCSEAYRYQVTPRMLCAGYRKG
KKDACQGDGGGPLVCKALSGRWFLAGLVSWGLGCGRPNYFGVYTRITGVISWIQQVVT
```

**Important features:**

**Type II transmembrane domain:**

amino acids 46-67

**Serine proteases, trypsin family, histidine active site.**

amino acids 604-609

**N-glycosylation sites.**

amino acids 127-130, 175-178, 207-210, 329-332, 424-427, 444-447  
and 509-512

**Kringle domains.**

amino acids 746-758 and 592-609

**Homologous region to Kallikrein Light Chain:**

amino acids 568-779

**Homologous region to Low-density lipoprotein receptor:**

amino acids 451-567

## FIGURE 64

GCACCCAGGCCAGTGGACGATCCAGAACAGGAGGCTGTGTGGCTTGCACATCCTGCAGCCC  
TACGCCGAGAGGATCCCCGTGGTGGCACGGCCGGGATCACCATCAACTCACCTCCAGAT  
CTCCCTCACCGGGCCCGGTGCGGGTGCACATGGCTTGACAACCAGTCGGACCCCTGCC  
CTGGAGAGTTCCCTCTGTTCTGTGAATGGACTCTGTGTCCCTGCCTGTGATGGGTCAAGGAC  
TGCCCCAACGGCCTGGATGAGAGAAACTGCCTTGCAGAGCCACATTCCAGTGCAGGAAAGAGGA  
CAGCACATGCATCTCACTGCCAAGGTCTGTGATGGCAGCCTGATTGTCTAACGGCAGCG  
ATGAAGAGCAGTGCCAGGAAGGGTGCCATGTGGACATTCACCTCCAGTGTGAGGACCGG  
AGCTGCGTAAGAACGCCAACCGCAGTGTGATGGCGGCCGACTGCAGGGACGGCTCGGA  
TGAGGAGCACTGTGACTGTGGCCTCCAGGGCCCTCCAGCCGCATTGTTGGAGCTGTGT  
CCTCCGAGGGTGAGTGGCCATGGCAGGCCAGCCTCCAGGTTGGTCGACACATCTGTGG  
GGGCCCTCATCGCTGACCGCTGGTGATAACAGCTGCCACTGCTTCCAGGAGGACAGCAT  
GGCCTCCACGGTGCTGTGGACCGTGTCCCTGGCAAGGTGTGGCAGAACTCGCCTGGCCTG  
GAGAGGTGTCTTCAGGTGAGCCGCTGCTGCAGCTCGACCACCCGGTGGCGCTGGCCCGTGC  
GAACGACGTGGCGCTGCTGCAGCTCGACCACCCGGTGGCGCTGGCCCGTGC  
CGTCTGCCTGCCCGCGCTCCACTTCTGAGCCCGCCTGCACTGCTGGATTACGGCT  
GGGCGCCTGCGCGAGGGCGCCCATCAGCAACGCTCTGCAGAAAAGTGGATGTGCAGTTG  
ATCCCACAGGACCTGTGCAGCGAGGCCTATCGCTACCAGGTGACGCCACGCATGCTGTG  
CGGCTACCGCAAGGGCAAGAAGGATGCCTGTCAGGGTACTCAGGTGGTCCGCTGGTGTG  
AGGCACTCAGTGGCCGCTGGTCTGGCGGGGCTGGTCAGCTGGGCGCTGGCTGGCCGG  
CCTAACTACTTCGGCGTCTACACCCGCATCACAGGTGTGATCAGCTGGATCCAGCAAGTGG  
GACCTGAGGAAC TGCCCCCTGCAAAGCAGGGCCCACCTCCTGGACTCAGAGAGCCAGGGC  
AACTGCCAAGCAGGGGACAAGTAT

## **FIGURE 65**

GGACGAGGCAGATCTCGTTCTGGGCAGCCGTTGACACTCGCTCCCTGCCACCGCCCCGGG  
CTCCGTGCCAAGTTTCATTTCACCTCTGCCTCCAGTCCCCCAGCCCCCTGGCCG  
AGAGAAGGGTCTTACCGGCCGGATTGCTGGAAACACCAAGAGGTGGTTTGTTTAAA  
ACTTCTGTTCTGGGAGGGGGTGTGGCGGGCAGGATGAGCAACTCCGTTCTGCTCTG  
TTTCTGGAGCCTCTGCTATTGCTTGCTGCCGGAGCCCCGTACCTTGGTCCAGAGGGAC  
GGCTGGAAGATAAGCTCCACAAACCAAAGCTACACAGACTGAGGTCAAACCATCTGTGAGG  
TTAACCTCCGCACCTCCAAGGACCCAGAGCATGAAGGATGCTACCTCTCCGTCGCCACAG  
CCAGCCCTAGAAGACTGCAGTTCAACATGACAGCTAAAACCTTTCATCATTACGGAT  
GGACGATGAGCGGTATCTTGAAACTGGCTGCACAAACTCGTGTCAAGCCCTGCACACAAGA  
GAGAAAGACGCCAATGTAGTTGTGGTTGACTGGCTCCCCCTGGCCACCAGCTTACACGGA  
TGCGGTCAATAATACCAGGGTGGTGGACACAGCATTGCCAGGATGCTGACTGGCTGCAGG  
AGAAGGACGATTTCTCTCGGAATGTCCACTTGATGGCTACAGCCTCGGAGCGCACGTG  
GCCGGGTATGCAGGCAACTCGTGAAGGAACGGTGGCCGAATCACAGGTTGGATCCTGC  
CGGGCCCATGTTGAAGGGGCCGACATCCACAAGAGGCTCTCCGGACGATGCAGATTTG  
TGGATGTCCACACCTACACGCGTTCTCGGCTTGAGCATTGGTATTAGATGCCTGTG  
GGCCACATTGACATCTACCCAAATGGGGTGACTTCCAGCCAGGCTGTGGACTAACGATGT  
CTTGGGATCAATTGCATATGGAACAATCACAGAGGTGGTAAATGTGAGGATGAGCGAGCCG  
TCCACCTTTGTTGACTCTCTGGTAATCAGGACAAGCCGAGTTGCCTCCAGTGCACT  
GACTCCAATCGTTCAAAAGGGATCTGTCTGAGCTGCCAAGAACCGTTGTAATAGCAT  
TGGCTACAATGCCAAGAAAATGAGGAACAAGAGGAACAGCAAATGTACCTAAAAACCGGG  
CAGGCATGCCCTTCAGAGGTAACCTCAGTCCCTGGAGTGTCCCTGAGGAAGGCCCTTAATA  
CCTCCTTCTTAATACCATGCTGCAGAGCAGGGCACATCCTAGCCCAGGAGAAGTGGCCAGCA  
CAATCCAATCAAATCGTTGCAAATCAGATTACACTGTGCATGTCTTAGGAAAGGAAATCTT  
ACAAAATAAACAGTGTGGACCCCTAATAAAAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAA

## FIGURE 66

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49646
><subunit 1 of 1, 354 aa, 1 stop
><MW: 39362, pI: 8.35, NX(S/T): 2
MSNSVPLLCFWSLCYCFAAGSPVPFGPEGRLEDKLHKPKATQTEVKPSVRFLRTSKDPEHE
GCYLSVGHSQPLEDCSFNMTAKTFFIIHGWTMSGIFENWLHKLVSALHTREKDANVVVDWL
PLAHQLYTDAVNNTRVVGHSIARMLDWLQEKKDDFSLGNVHLIGYSLGAHVAGYAGNFVKGT
GRITGLDPAGPMFEGADIHKRLSPDDADFVDVLHTYTRSGFLSIGIQMPVGHIDYPNGGDF
QPGCGLNDVLGSIAYGTITEVVKCEHERAVHLFVDSLNVQDKPSFAFQCTDSNRFKKGICL
CRKNRCNSIGYNAAKKMRNKRNSKMYLKTRAGMPFRGNLQSLECP
```

**Important features:**

**Signal peptide:**

amino acids 1-16

**Lipases, serine active site.**

amino acids 163-172

**N-glycosylation sites.**

amino acids 80-83 and 136-139

## FIGURE 67

CGGACGCGTGGCGGACCGTGGGCCTGGCAAGGGCGGGCGCCGGCGAGCCACCTTCCCCCTCCCCCGC  
TTCCCTGTGCGCTCCGCTGGCTGGACCGCCTGGAGGAGTGGAGCAGCACCCGCCGGCCCTGGGGCTGACAGT  
CGGAAAGTTGGCCGAAGAGGAAGTGGCTCAAACCCGGCAGGTGGGACCCAGGGCCAGACCAGGGCGCTCG  
CTGCCTGCGGGCGGGCTGTAGGCGAGGGCGCCCCAGTGCGAGACCCGGGCTTCAGGAGCCGGCCCCGGAG  
AGAAGAGTGGCGGGCGACGGAGAAAACAACCTCAAAGTTGGCAGAAGGCACCGCCCTACTCCCAGGGCTGCC  
CCGCCTCCCCGGCCCGAGCCCTGGCATCCAGACTACGGGTCGAGCCGGGCGATGGAGCCCCCTGGGAGGCC  
CACCAGGGAGGCTGGGCGCCGGGCTCCGCCCGACCCATGGGTAGACCAAGAAGCTCCGGGACCCCTCC  
GCACCTCTGGACAGCCAGGATGCTTGGCACCCCTCCCTCCCTGGAGGCCTGGCCATCCAG  
ACCGGATTATTTCAAATCATGCTGTGAGGACCCCCCAGCAGTGCTTAAAGTGCAGGGCACCTACAGA  
GGCCCTGGTCCGGGACAGCGCACCTCCCTGCCAACCTGCACCTGGCTCATCCTGGCAGCAAGGAACAGACTG  
TCACCATCAGGTTCCAGAAGCTACACCTGGCTGTGGCTCAGAGCCTTAACCCCTACGCTCCCTCCAGGCC  
TGATCTCCCTGTGTGAGGCACCTCCAGCCCTTGCAAGCTGCCGGGGCAACGTACCATCACTACAGCTATG  
CTGGGCCAGAGCACCCATGGCCAGGGCTTCTGCTCCCTACAGCCAAGATTGGCTATGTGCCCTGCAGGAAG  
AGTTTCAGTGCCTGAACCACCGCTGTATCTGCTGTCCAGCCTGTGATGGGTTGATGCCCTGTGGCAGTGGCT  
CTGATGAAGCAGGTTGCAGCTCAGACCCCTTCCCTGGCTGACCCCAAGACCCGCTCCCTGCCCTGCAATG  
TCACCTTGGAGGACTTCATGGGTCTTCTCTCTGGATATAACACACCTAGCCTCAGTCTCCCACCCCCAGT  
CCTGCCATTGGCTGCTGGACCCCCATGATGGCCGGCGCTGGCGTGCCTCACAGCCCTGGACTTGGGCTTTG  
GAGATGCAAGGCTGACTGTGAGACACTGCTGGCAGGCTGTGCTTACACACAGTGGCTTAGTCTCACCCACTTCA  
GCAATGGCAAGGCTGACTGTGAGGAGACACTGCTGGCAGGCTGTGCTTACACACAGTGGCTTAGGAGCA  
ATGGTCGTGGCTCAATGCCACCTACATGTGCGGGCTATTGCTTGGCTTGGGACAGACCCCTGTGGCTTAGGCT  
CTGGCCTGGGAGCTGGCGAAGGCCCTAGGTGAGGCGCTACAGTGAGGACAGCGCTGTGACGGCTATGGGACT  
GTGCTGACGGCACAGATGAGGAGACTGCCAGGCTGCCCACCTGGACACTTCCCTGTGGGCTGTGGCACCT  
CTGGTGCCACAGCTGCTACCTGCTGACCGCTGCAACTACAGACTTTCTGTGCTGATGGAGCAGATGAGA  
GAGCTGTCGGCATTGCCAGGCTGGCAATTCCGATGCCGGGACGAGAAGTGGCTGTGAGACGTGGGTGCG  
ATGGGAGCCAGACTGTGCGGACGGCAGTGATGAGTGGACTGCTCTATGTTCTGCCCGCAAGGTCAATTACAG  
CTGAGTCATTGGCAGCTAGTGTGCGGCTGCTCTGGTCATGCCCTGGGCTGCACCTGCAAGCTCTATGCCA  
TTCGCACCCAGGAGTACAGCATCTTGCCCCCCTCTCCCGATGGAGGCTGAGATTGTGCAAGCAGGCAACCC  
CTTCCTACGGCAGCTCATTGCCAGGCTGCCATCCCACCTGTAGAAGACTTCTACAGAGAACTCTAATGATA  
ACTCAGTGTGGCAACCTGCGTTCTGCTACAGATCTACGCCAGGATATGACTCCAGGAGGTGGCCAGGTG  
CCGCCGTCGTGAGGCCCTGGTACGCCCTGCCGCTGGGCTTGCTCCCTGAA  
CCAACACCCGGCTCGGCCCTGAGGCCAGATCCAGGTCACACCTCTGCTGCTCCCTGAGGCCCTAGATG  
GTGGCACAGGCTCAGCCGTGAGGCCGGGAGTGGGTGGCAAGATGGGAGCAGGCCACCCACTGCCATCA  
AGGCTCCCTCCCATCTGCTAGCACGTCTCCAGCCCCACTACTGTCCTGAAGGCCAGGGCCACTGCCCTCAC  
TGCCCTAGAGCCATCACTATTGCTGGAGTGGTGCAGGCCCTGCCAGGCCGCTGGCCAGGCCCTGGGGCC  
CAGGACCAACCCGGAGGCCCTGAGGCCACACAGCAGTCCTGGCCCTGGAAGATGAGGACGATGTGCTACTGG  
TGCACTGGCTGAGGCCGGGAGTGGTAGCTGAGGCCAGGAGTGGCCACTGCTTACCTTGAGGGACCTGGGG  
CTCTACTGAGGCCCTCTCCCTGGGGCTCTACTCATAGTGGCACAAACCTTTAGAGGTGGGTAGCCTCCCTC  
ACCAACTTCCCTCCCTGGATTTCAGGGACTTGGTGGGCCCTCCGGTTGACCCCTATGTAGCTGCTATAAAGT  
TAAGTGTCCCTCAGGCAGGGAGAGGGCTCACAGACTCCTCTGTACGTGGCCATGGCCAGACACCCAGTCC  
TCACCAACCATGCTCCCAACGCCACCATTTGGGTGGCTGTTTAAAGTAAAGTCTTAGAGGATCATA  
GGTCTGGACACTCCATCCTGCCAACCTCACCCAAAAGTGGCCTTAAGCACCAGGAATGCCAATTAACTAGAGA  
CCCTCCAGCCCCAAGGGAGGATTGGCAGAACCTGAGGTTTGGCATCCACAATCCCTACAGGGCTGG  
CTCACAAAAAGAGTGCAACAAATGCTTCTATTCCATAGCTACGGCATTGCTAGTAAGTTGAGGTAAAAATAAA  
GGAATCATACTCTC

## FIGURE 68

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49631
<subunit 1 of 1, 713 aa, 1 stop
<MW: 76193, pI: 5.42, NX(S/T): 4
MLLATLLLLLGGALAHPDRIIFPNHACEDPPAVLLEVQGTLQRPLVRDSRTSPANCTWLIL
GSKEQTVTIRFQKLHLACGSERLTLRSPLQPLISLCEAPPSPQLPGGNVTITYSYAGARAP
MGQGFLLSYSQDWLMCLQEEFQCLNHRCVSAVQRCGVDAACGDGSDEAGCSSDPFPGLTPRP
VPSLPCNVTLEDFYGVFSSPGYTHLASVSHPQSCHWLLDPHDGRRLAVRFTALDLGFGDAVH
VYDGPgpPESSRLLRSLTHFSNGKAVTVETLSGQAVVSYHTVAWSNGRGFNATYHVRGYCLP
WDRPCGLGSGLGAGEGLGERCYSEAQRCDGSWDCADGTDEEDCPGCPPGHFPCGAAGTSGAT
ACYLPADRCNYQTFCADGADERRCRHCQPGNFRCRDEKCVYETWVCDGQPDCAAGSDEWDGS
YVLPRKVITAAVIGSLVCGLLVIALGCTCKLYAIRTQEYSIFAPLSRMEAEIVQQQAPPSY
GQLIAQGAIAPPVEDFTPENPNDNSVLDNLRSLLQILRQDMTPGGPGARRQRGRILMRRLLVR
RLRRWGLLPRTNTPARASEARSQVTPSAAPLEALDGGTGPAREGGAVGGQDGGEQAPPLPIKA
PLPSASTSPAPTTVPEAPGPLPSLPLEPSLLSGVVQALRGRLPSLGPPGptrsppgptav
LALEDEDVLLVPLAEPGVWVAEAEDEPLLT
```

**Important features:**

**Signal peptide:**

amino acids 1-16

**Transmembrane domain:**

amino acids 442-462

**LDL-receptor class A (LDLRA) domain proteins**

amino acids 411-431, 152-171, 331-350 and 374-393

## FIGURE 69

CGAGCTGGCGAGAAGTAGGGGAGGGCGGTGCTCCGCCGCGTGGCGGTGCTATCGCTTCG  
CAGAACCTACTCAGGCAGCCAGCTGAGAAGAGTTGAGGGAAAGTGCTGCTGGGTCTGCA  
GACGCGATGGAATAACGTGCAGCCGAAAATAAAACATCGCCCCTCTGCTTCAGTGTGAAAGG  
CCACGTGAAGATGCTGCGGCTGGCACTAACTGTGACATCTATGACCTTTTATCATGCAC  
AAGCCCCTGAACCATAATTGTTATCACTGGATTGAAGTCACCGTTATCTTATTTTCATA  
CTTTTATATGTACTCAGACTTGATCGATTAATGAAGTGGTTATTTGGCCTTGCTTGATAT  
TATCAACTCACTGGTAACAACAGTATTCA TGCTCATCGTATCTGTGTTGGCACTGATACCAG  
AAACCACAAACATTGACAGTTGGTGGAGGGGTGTTGCAC TTGTGACAGCAGTATGCTGTCTT  
GCCGACGGGCCCTTATTTACCGGAAGCTTCTGTTCAATCCCAGCGGTCTTACCAAGAAAAAA  
GCCTGTGCATGAAAAAAAAGAAGTTTGTATTTATATTACTTTAGTTGATAACTAAGT  
ATTAACATATTCTGTATTCTTCAAAAAAAAAAAAAAAA

## FIGURE 70

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49645
><subunit 1 of 1, 152 aa, 1 stop
><MW: 17170, pI: 9.62, NX(S/T): 1
MDNVQPKIKHRPFCFSVKGHVKMLRLALTTSMTFFIIAQAPEPYIVITGFEVTVILFFILL
YVLRLDRLMKWLFWPPLLDIINSLVTTVFMLIVSVLALIPETTTLTVGGGVFALVTAVCCLAD
GALIYRKLLFNPSGPYQKKPVHEKKEVL
```

**Important features:**

**Potential type II transmembrane domain:**

amino acids 26-42

**Other potential transmembrane domain:**

amino acids 44-65, 81-101 and 109-129

**Leucine zipper pattern**

amino acids 78-99 and 85-106

**N-myristoylation site.**

amino acids 110-115

**Ribonucleotide reductase large subunit protein**

amino acids 116-127

## **FIGURE 71**

GGCGAGAAGTAGGGAGGGCGTGTCCGCCGCGGTGGCGGTGCTATCGTTTGACAGAAC  
TACTCAGGCAGCCAGNTGAGAAGAGTTGAGGGAAAGTGCTGCTGGGTCTGCAGACGCGA  
TGGATAACGTGCAGCCGAAAATAAAACATGCCCTCTGCTTCAGTGTGAAAGGCCACGTG  
AAGATGCTGCGGCTGGCACTAACTGNGACATCTATGACCTTTTATNATCGCACAAGCCCC  
TGAACCATAATTGTTATCACTGGATTGAAGTCACCGTTATCTTATTTTCTACATTTTAT  
ATGTACTCAGACTTGATCGATTAATGAAGTGGTTATTTGGCCTTGCTGATATTATCAAC  
TCACTGGTAACAACAGTATTGCTCATCGTATCTGTGTTGGCACTGATACCAGAAACCAC  
AACATTGACAGTTGGTGGAGGGGTGTTGCACTTGTGACAGCAGTATGCTGTNTGCCGAC

## FIGURE 72

CAGCCCCGCGCGCCGGCGAGTCGCTGAGCCGGCTGCCGGACGGGACGGGACCGGCTAGG  
CTGGGCGC~~CCCCCCC~~GGGCCGTGGCATGGCGACTGGCCGGCTGCTGCTGC  
CTCTGCTGGCCCAGTGGCTCCTGCGCCGCCGGAGCTGGCCCCGCGCCCTCACGCTG  
CCCCTCCGGGTGGCCGCCACGAACCACGTAGTTGCGCCCACCCGGACCCGGACCCC  
TGCCGAGGCCACGCCGACGGCTTGGCGCTGCCCTGGAGCCTGCCCTGGCGTCCCCGG  
GCGCCGCCAACCTCTTGGCCATGGTAGACAACCTGCAGGGGACTCTGGCCGGCTACTAC  
CTGGAGATGCTGATCGGGACCCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAG  
TAACCTTGCCGTGGCAGGAACCCGCACTCCTACATAGACACGTACTTGACACAGAGAGGT  
CTAGCACATACCGCTCCAAGGGCTTGACGTACAGTGAAGTACACACAAGGAAGCTGGACG  
GGCTTCGTTGGGAAGACCTCGTCACCACCCAAAGGCTCAATACTTCTTCTGTCAA  
CATTGCCACTATTTGAATCAGAGAATTCTTTGCCTGGATTAAATGGAATGGAATAC  
TTGGCCTAGCTTATGCCACACTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTCGACTCC  
CTGGTACACAAGCAAACATCCCAACGTTCTCCATGCAGATGTGTGGAGCCGGCTGCC  
CGTTGCTGGATCTGGACCAACGGAGGTAGTCTTGTCTGGGTGGAATTGAACCAAGTTGT  
ATAAAGGAGACATCTGGTATAACCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTG  
AAATTGGAAATTGGAGGCCAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGC  
CATCGTGGACAGTGGCACCACGCTGCGCCTGCCAGAAGGTGTTGATGCGGTGGTGG  
AAGCTGTGCCCGCGCATCTGATTCCAGAATTCTCTGATGGTTCTGGACTGGGTCCCAG  
CTGGCGTGTGGACGAATTGGAAACACCTTGGCTTACTTCCCTAAATCTCCATCTACCT  
GAGAGACGAGAACTCCAGCAGGTATTCCGTATCACAACTCCTGCCTCAGCTTACATTAGC  
CCATGATGGGGCCGGCCTGAATTATGAATGTTACCGATTGGCATTCCCCATCCACAAAT  
GCGCTGGTATGGTGCACGGTATGGAGGGCTTACGTATCTCGACAGAGCCCAGAA  
GAGGGTGGCTTCGCGAGCGAGCCCTGTGCAGAAATTGCGAGGTGCTGCAGTGTCTGAAATT  
CCGGGCCTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCGCTCAGTCTTGAGCGAG  
CCCATTGTGGATTGTGTCTATGCGCTCATGAGCGTCTGTGGAGCCATCCTCTGTCTT  
AATCGTCCTGCTGCTGCGTCCGGTGTCAAGCGTCGCCCGTGACCCCTGAGGTGTC  
ATGATGAGTCCTCTGGTCAGACATCGCTGGAAATGAATAGCCAGGCCTGACCTCAAGCAA  
CCATGAACTCAGCTATTAAGAAAATCACATTCCAGGGCAGCAGCCGGATCGATGGTGGCG  
CTTCTCCTGTGCCACCCGTCTCAATCTCTGTTCTGCTCCAGATGCCTCTAGATTAC  
TGTCTTTGATTCTGATTTCAGCTTCAAATCCTCCACTTCCAAGAAAAATAATTAA  
AAAAAAAACTTCATTCTAA

## **FIGURE 73**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45493
><subunit 1 of 1, 518 aa, 1 stop
><MW: 56180, pi: 5.08, NX(S/T): 2
MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAATNRVVAPTPGPGTPAERHADGLAL
ALEPALASPAGAANFLAMVDNLQGDSGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTPHS
YIDTYFDTERSSTYRSKGFDVTVKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATIFESENF
FLPGIKWNGILGLAYATLAKPSSLETFFDSLVTQANI PNVFSMQMCGAGLPVAGSGTNGGS
LVLGGIEPSLYKGDIWYTPIKEEWYYQIEILKLEIGGQSLNLDREYNADKAIVDSGTTLLR
LPQKVFDAVVEAVARASLIPEFSDGFWTGSQLACWTNSETPWSYFPKISIYLRDENSSRSFR
ITILPQLYIQPMMGAGLNYE CYRGISPSTNALVIGATVMEGFYVIFDRAQKRVGFAASPCA
EIAGAAVSEISGPFSTEDVASNCVPAQSLSEPILWIVSYALMSVC GAILLV LIVLLL PFRC
QRPRDPEVVNDESSLVRHRWK
```

**Important features:**

**Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 466-494

**N-glycosylation sites.**

amino acids 170-173 and 366-369

**Leucine zipper pattern.**

amino acids 10-31 and 197-118

**Eukaryotic and viral aspartyl proteases**

amino acids 109-118, 252-261 and 298-310

## FIGURE 74

CGCCTCCGCCTCGGAGGCTGACGCGCCGGCGCCGTTCCAGGCCTGTGCAGGGCGGATCG  
GCAGCCGCCTGGCGGCATCCAGGGCGGTGCGGGGCCTGGCGGGAGCCGGAGGCCGGCC  
**GGCATGGAGGCCTGCTGCTGGCGCGGGTTGCTGCTGGCGCTTACGTCTTGCTACTA**  
CAACCTGGTGAAGGCCCGCCGTGCGGCCGATGGCAACCTGCGGGGCCACGGCGTGG  
TCACGGGCCAACAGCGGCATCGAAAGATGACGGCGCTGGAGCTGGCGGCCGGAGCG  
CGCGTGGTGCCTGGCGCCAGCCAGGAGCGCGGGAGGCCTGCCTCGACCTCCGCCA  
GGAGAGTGGAAACAATGAGGTCATCTCATGGCCTTGGACTTGGCAGTCTGGCCTCGGTGC  
GGGCCTTGCCACTGCCTTCTGAGCTTGAGCCACGGTTGGACATCCTCATCCACAATGCC  
GGTATCAGTTCTGTGGCGGACCGTGAGGCCTTAACCTGCTGCTCGGGTGAACCATA  
CGGTCCCTTCTGCTGACACATCTGCTGCCTGCCTGAGGCATGTGCCCTAGCCGCG  
TGGTGGTGGTAGCCTCAGCTGCCACTGTCGGGACGTCTGACTCAAACGCCTGGACCGC  
CCAGTGGTGGCTGGCGCAGGAGCTGCGGCATATGCTGACACTAACGCTGGCTAATGTACT  
GTTTGCCTGGGAGCTGCCAACAGCTTGAGGCCACTGGCGTCACCTGCTATGCAGCCCACC  
CAGGGCCTGTGAACTCGGAGCTGTTCTGCGCATGTTCTGGATGGCTGCCACTTTG  
CGCCCATTGGCTTGCTGGCTCCGGCACCAAGAGGGGTGCCAGACACCCCTGTATTG  
TGCTCTACAAGAGGGCATCGAGCCCTCAGTGGAGATATTTGCCACTGCCATGTGGAAG  
AGGTGCCTCCAGCTGCCGAGACGACCGGGCAGCCATGGCTATGGGAGGCCAGCAAGAGG  
CTGGCAGGGCTGGGCTGGGAGGATGCTGAACCCGATGAAGACCCCCAGTCTGAGGACTC  
AGAGGCCCATCTCTCTAACGACCCCCCACCTGAGGAGCCCACAGTTCTAACCTTACC  
CCAGCCCTCAGAGCTCACCAGATTGTCTAACGACGACCGAATTCAAGCTAAAGTTGAG  
CCTGAGATCCAGCTCTCC**TAA**CCCTCAGGCCAGGATGCTGCCATGGCACTTCATGGCCTT  
GAAAACCTGGATGTGTGAGGCCATGCCCTGGACACTGACGGTTGTGATCTGACCTC  
CGTGGTTACTTCTGGGCCCAAGCTGTGCCCTGGACATCTCTTCTGGTGAAGGAAT  
AATGGGTGATTATTCCTCTGAGAGTGACAGTAACCCAGATGGAGAGATAGGGTATGCT  
AGACACTGTGCTTCGGAAATTGGATGTAGTATTTCAAGGCCAACCCCTATTGATTCTG  
ATCAGCTCTGGAGCAGAGCAGGGAGTTGCAATGTGATGCAGTGCACACATTGAGAATTAG  
TGAACATGATCCCTTGCAACCGTCTAGCTAGGTAGTTAAATTACCCCATGTTAATGAAGCG  
GAATTAGGCTCCCGAGCTAAGGGACTCGCCTAGGGTCTCACAGTGAGTAGGAGGAGGGCCTG  
GGATCTGAACCCAAGGGTCTGAGGCCAGGGCAGTGCCTAAGATGGGTGCTGAGAAGTGA  
GTCAGGGCAGGGCAGCTGGTATCGAGGTGCCCATGGAGTAAGGGACGCCCTCCGGCGG  
ATGCAGGGCTGGGTCACTGTATCTGAAGCCCTCGGAATAAGCGCGTTGACCGCCAAA  
AAAAAAAAAAAAAAA

## **FIGURE 75**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48227
<subunit 1 of 1, 377 aa, 1 stop
<MW: 40849, pI: 7.98, NX(S/T): 0
MEALLLGAGLLLGYLVYYNLVKAPPCCGGMGNLRGRTAVVTGANSIGKMTALELARRGAR
VVLACRSQERGEAAAFDLRQESGNNEVIFMALDLASLASVRAFATAFLSSEPRLDILIHNAG
ISSCGRTREAFNLLRVNHIGPFLTHLLPCLKACAPSRRVVVVASAAHCRGRDFKRLDRP
VVGWRQELRAYADTKLANVLFARELANQLEATGVTCYAAHPGPVNSELFRLHVPGWLRPLLR
PLAWLVLRAPRGGAQTPLYCALQEGIEPLSGRYFANCHVEEVPPAARDRAAHRLWEASKRL
AGLGPGEDAEPDEDPQSEDSEAPSSLSTPHPEEPTVSQPYPSHQSSPDLSKMTHRIQAKVEP
EIQLS
```

**Important features:**

**Signal peptide:**

amino acids 1-16

**Glycosaminoglycan attachment site.**

amino acids 46-49

**Short-chain alcohol dehydrogenase family**

amino acids 37-49 and 114-124

## FIGURE 76

GGAGGAGACAGCCTCCTGGGGCAGGGTCCCTGCCTCTGCTGCTCTGCTCATC**ATGGGAGGCATGGCTCAG**  
GACTCCCCGCCAGATCTAGTCCACCCCCAGGACCAGCTGTTCCAGGGCCCTGGCCAGGATGAGCTGC  
CAAGCCTCAGGGCAGCCACCTCCCACCATCCGTGGTGTGAATGGGAGCCCTGCCAGGATGGCTGC  
CCACACCACCTCCTGCCTGATGGGACCCCTCTGCTACAGCCCCCTGCCCGGGACATGCCACGATGGCCAG  
GCCCTGTCCACAGACCTGGGTGTCTACACATGTGAGGCCAGCAACGGCTTGGCACGGCAGTCAGCAGAGGCCT  
CGGCTGTCTGGCTGTCTCCGGGAGGATTCCAGATCCAGCCTGGACATGGTGGCTGTGGTGGGTGAGCAG  
TTTACTCTGGAATGTGGGCCCTGGGCCACCCAGAGCCCACAGTCTCATGGTGGAAAGATGGGAAACCCCTG  
GCCCTCCAGCCCGAAGGCACACAGTGTGGGGGTCCCTGCTGATGGCAAGAGCAGAGAAGACTGACGAAGGG  
ACCTACATGTGTGGCCACCAACAGCGCAGGACATAGGGAGAGGCCCGCAGCCGGTTTCCATCCAGGAGCCC  
CAGGACTACACGGAGGCCTGTGGAGCTTCTGGCTGTGCAATTCACTGCTGAAAATGTGACACTGCTGAACCCGGAT  
CCTGCAGAGGGCCCAAGCCTAGACCGCGGTGTGGCTCAGCTGGAAGGTCAGTGGCCCTGCTGCGCCTGCCAA  
TCTTACACGGCCTGTTAGGACCCAGACTGCCCGGGAGGCCAGGGAGCTCCGTGGCAGAGGAGCTGCTGGCC  
GGCTGGCAGAGCGCAGAGCTGGAGGCCTCCACTGGGCCAAGACTACAGAGTTCAAAGTGAGGACCATCTCTGGC  
CGGGCTCGAGGCCCTGACAGCAACGTGCTGCTCTGAGGTGCGGAAAAAGTGCCAGTGCCACCTCAGGAA  
GTGACTCTAAAGCCTGGCAATGGCACTGTCTTGTGAGCTGGTCCACCTGCTGAAAACCACAATGGCATE  
ATCCGTGGCTACCAGGTCTGGAGCTGGCAACACATCACTGCCACAGCCAACGGACTGTAGTTGGTGAGCAG  
ACCCAGCTGGAATGCCACCCATATGCCAGGTCTCTACTGCGTGCAAGTGGCTGCAGTCAGTGGTGCTGGAGCT  
GGGGAGGCCAGTAGACCTGCTGCCCTTTAGAGCAGGCCATGGAGCGAGGCCACCCAAGAACCCAGTGAGCAT  
GGTCCCTGGACCCCTGGAGCAGCTGAGGGCTACCTTGAGCGGCCTGAGGTATTGCCACCTGCGGTGTTGCACTC  
TGGCTGTGCTCTGGGACCCGGCGTGTGTATCCACCGCCGGCGCCAGCTAGGGTGCACCTGGGCCAGGTCTG  
TACAGATAACAGTGGAGATGCCATCTAAAACACAGGATGGATCACTGAGCTCCCAGTGGTGGCAGAGACACT  
TGGCTTCCACCTCTGGCTCTGGGACCTGAGCAGCAGCAGCAGCAGCCCTCAGCAGTCGGCTGGGGCGGATGCCCG  
GACCACTAGACTGTCGTCGCTCTGAGCTCCACCGCCGGCGCCAGCTAGGGTGCACCTCCAGACACC  
AGCACTTTTATGGCTCCCTCATCGTGAGCTGCCCTCCAGTACCCAGGCCAGGCAAGTCCCAGGTCCAGCT  
GTCAGGCCCTCCCACCCAGCTGGCCAGCTCTCCAGCCCCCTGTTCCAGCTCAGACAGCCTCTGCAAGCCGAGG  
GGACTCTCTCTCCCGCTTGTCTCTGGCCCTGAGGGCTTGGAGGCCAAAAGAAGCAGGAGCTGCAGCAT  
GCCAACAGTTCCCCTGCTCCGGGCAGCCACTCTTGAGCTCCGGCTGTGAGTTAGGAAATAGAGGTCC  
AAGAACCTTCCAAAGCCCAGGAGCTGTGCCCAAGCTCTGGTGCCTGGGGCCCTGGGACCGAAACTCCTC  
AGCTCCTCAAATGAGCTGGTTACTCGTCATCTCCCTCCAGCACCCCTTTCTCATGAAACTCCCCAACTCAG  
AGTCACACAGACCCAGCCTCCGGTGGCACCACAGGCTCCCTCCATCCTGCTGCCAGCAGCCCCCATCCCCATC  
CTTAGCCCTGCACTCCCCCTAGCCCCCAGGCCTCTCCCTCTGCCCCAGCCAGCTCCAGTCGCTGTCC  
AGCTCCTCACTGTCATCCCTGGGGAGGATCAAGACAGCGTGTGACCCCTGAGGAGTAGCCCTGTGCTTGAA  
CTCAGTGAGGGTGGAGGAGACTCCAGGAACAGCGTCTCCATGCAAGGGCTCCTCACCCCCCACCACCTAT  
GGGTACATCAGCGTCCCAACAGCCTCAGAGTTACGGACATGGCAGGACTGGAGGAGGGTGGGGCCAAGGGGG  
GGAGTCTTGCTGTGCCACCTCGGCCCTGCCCTACCCCCACCCCGAGCGAGGGCTCTTAGCCAATGGTTGGGGC  
TCAGCCTCTGAGGACAATGCCGCCAGCGCCAGGCCAGCTTGTCACTCCTCCGATGGCTCTTCCCTCGCTGAT  
GCTCACTTGGCCGGCCCTGGCAGTGGCTGGATAGCTTGGTTGGCTAGAGCCCAGGGAGGAGACTGC  
GTCCTCATAGATGCCCTCATCCTCTCCCTCCCCACGGGATGAGATCTCTGACCCCCAACCTCTCCCTGCCCC  
TGGGAGTGGAGGCCAGACTGGTTGGAAGACATGGAGGTCAGCCACACCCAGCGGCTGGGAAGGGGATGCCCT  
TGGGCCCCCTGACTCTGAGATCTCTCCCTGAGAGACTCCAGACGGGAATCAGAACCAACTTCTCTGCA  
GTAGATTACTCT**TGAACCGTGTCCCTGAGACTCTCCAGACGGGAATCAGAACCAACTTCTCTGCA**CCCCACAAG  
ACCTGGGCTGTGGTGTGGGTCTTGGCTGTGTTCTGCACTGGGTCACCTCCAGGAGGAGAGAG  
TTCTCCCTCCAGATTGTGAAAACAATGAAAACAAAATTAGAGCAAAGCTGACCTGGAGCCCTCAGGGAGCAA  
ACATCATCTCCACCTGACTCCTAGCCACTGCTTCTGCTGCACTCCACCCACCCAGGTTGTTTGGC  
CTGAGGAGCAGCCCTGCCGTGCTGCTCTTCCCCCACCATTGGATCACAGGAAGTGGAGGAGCCAGGGTGCCTT  
GTGGAGGACAGCAGTGGCTGCTGGAGAGGGCTGTGGAGGAAGGAGCTCTCGGAGCCCCCTCTAGCCTTACCT  
GGGGCCCTCCTCTAGAGAAGAGCTCAACTCTCTCCAAACCTCACCATGGAAAGAAAATAATTATGAATGCCACTG  
AGGCACTGAGGCCCTACCTCATGCCAAACAAAGGGTTCAAGGCTGGGTCTAGCGAGGATGCTGAAGGAAGGGAGG  
TATGAGACCGTAGGTCAAAGCACCACCTCGTACTGTTGTCATATGAGCTTAAGAAATTGATACCATAAAAT  
GGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## FIGURE 77

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA41404
<subunit 1 of 1, 985 aa, 1 stop
<MW: 105336, pI: 6.55, NX(S/T): 7
MGGMAQDSPPQILVHPQDQLFQGPGPARMSCQASGQPPPTIRWLLNGQPLSMVPPDPHLLP
DGTLQLLQPPARGHAHDGQALSTDLGVTCEASNRLGTAVSRGARLSAVLREDFOIQPRDM
VAVVGEQFTLECGPPWGHPEPTVSWWKDGKPLALQPGRHTVSGSLLMARAEEKSDEGYMCV
ATNSAGHRESRAARVSIQEPQDYTEPVELLAVRIQLENVTLLNPDPAEGPKPRPAVWLWKV
SGPAAPAQSYTALFRQTAPGGQGAPWAEELLAGWQSAELGGLHWGQDYEFKVRPSSGRARG
PDSNVLLLRLPEKVPAPPQEVTLKPGNGTVFVSWVPPAENHNGIIRGYQVWSLGNTSLPP
ANWTVVGEQTQLEIATHMPGSYCVQVAVTGAGAGEPSRPVCLLLEQAMERATQEPSEHGPW
TLEQLRATLKRPEVIATCGVALWLLLGTAVCIHRRRARVHLGPGLYRYTSEDAILKHRMD
HDSQWLADTWRSSTSGSRDLSSSSSLSRLGADARDPLDCRRSLLSDRSRSPGVPLL PDTST
FYGSLIAELPSSTPARPSPQVPAVRRLPPQLAQLSSPCSSSDSCLCSRRLGSSPRLSLAPAEA
WKAKKKQELQHANSPLLRGSHSLELRACELGNRGSKNLSQSPGAVPQALVAWRALGPKLLS
SSNELVTRHLPPAPLFPHETPPTQSQQTQPPVAPQAPSSILLPAAPIPILSPCSPPSPQASS
LSGPSPASSRLSSSSLSSLGEDQDSVLTPPEEVALCLELSEGEETPRNSVSPMPRAPSPTTY
GYISVPTASEFTDMGRTGGVGPKGGVLLCPRPCLTPSEGSILANGWGSASEDNAASARA
SLVSSSDGSFLADAHFARALAVAVDSFGGLEPREADCVFIDASSPPSPRDEIFLTPNLSLP
LWEWRPDWLEDMEVSHTQRLGRGMPPWPPDSQISSQRSQLHCRMPKAGASPVDYS
```

**Important features:**

**Transmembrane domain:**

amino acids 448-467

**N-glycosylation sites:**

amino acids 224-227, 338-341, 367-370, 374-377, 658-661 and 926-929

**N-myristoylation sites.**

amino acids 47-52, 80-85, 88-93, 99-104, 105-110, 181-186, 272-277, 290-295, 355-360, 403-408, 462-467, 561-566, 652-657, 849-854 and 876-881

**Phosphotyrosine interaction domain proteins**

amino acids 740-753

## FIGURE 78

CTCCCACGGTGTCCAGGCCAGAATGCGGCTCTGGCCTGCTATGGGTTGCCTGCTGCT  
CCCAGGTTATGAAGCCCTGGAGGGCCAGAGGAATCAGCGGGTCGAAGGGACACTGTGT  
CCCTGCAGTGCACCTACAGGAAGAGCTGAGGGACCACCGAAGTACTGGTCAGGAAGGGT  
GGGATCCTCTCTCGCTGCTGGCACCATCTATGCAGAAGAAGAAGGCCAGGAGACAAT  
GAAGGGCAGGGTGTCCATCCGTACAGCCAGGAGCTCGCTCATTGTGACCCGTGGA  
ACCTCACCTGCAAGACGCTGGGAGTACTGGTGTTGGTCGAAAAACGGGCCCCATGAG  
TCTTACTGATCTCTGTTCTGCTTCCAGGACCTGCTGCTCCCTCCCTCTCCCAC  
CTTCCAGCCTCTGGCTACAAACACGCCTGCAGCCAAGGAAAAGCTCAGCAAACCCAGCCCC  
CAGGATTGACTTCTCCTGGGCTTACCCGGCAGCCACCACAGCCAAGCAGGGAAAGACAGGG  
GCTGAGGCCCTCATTGCCAGGGACTTCCCAGTACGGCACGAAAGGACTTCTCAGTACAC  
AGGAACCTCTCCTCACCCAGCGACCTCTCCTGCAGGGAGCTCCGCCCCCCCATGCAGC  
TGGACTCCACCTCAGCAGAGGACACCAGTCAGCTCTCAGCAGTGGCAGCTCTAAGCCCAGG  
GTGTCCATCCCGATGGTCCGCATACTGGCCCCAGTCCTGGTGTGCTGAGCCTTGTGAGC  
CGCAGGCCTGATGCCCTCTGCAGCCACCTGCTCTGGAGAAAGGAAGCTAACAGGCCA  
CGGAGACACAGAGGAACGAGAAGTTCTGGCTCTCACGCTTGACTGCGGAGGAAAAGGAAGCC  
CCTTCCCAGGCCCTGAGGGGACGTGATCTCGATGCCCTCCACACATCTGAGGAGGA  
GCTGGGCTTCTGAAGTTGTCTCAGCGTAGGGCAGGAGGCCCTCTGGCCAGGCCAGCAGT  
GAAGCAGTATGGCTGGCTGGATCAGCACCGATTCCGAAAGCTTCCACCTCAGCCTCAGAG  
TCCAGCTGCCGGACTCCAGGGCTCTCCCCACCCCTCCCAGGCTCTCCTTGATGTTCCA  
GCCTGACCTAGAACGCTTGTCAAGCCCTGGAGGCCAGAGCGGTGGCTTGCTCTCCGGCTG  
GAGACTGGGACATCCCTGATAGGTTCACATCCCTGGGAGACTACCAAGGCTGCTGACCCCTCA  
GCAGGGCCAGACAAGGCTCAGTGGATCTGGTCTGAGTTCAATCTGCCAGGAACTCCTGGC  
CTCATGCCCTAGTGTGGACCCCTGCCTCCCTCCACTCCAGACCCACCTTGTCTTCCCTCC  
TGGCGTCTCAGACTTAGTCCCACGGTCTCCTGCATCAGCTGGTGTGAAGAGGGAGCATGCT  
GGGGTGAGACTGGGATTCTGGCTTCTTTGAACCACCTGCATCCAGCCCTCAGGAAGCCT  
GTGAAAACGTGATTCCCTGGCCCCACCAAGACCCACCAAAACCATCTCTGGGCTTGGTGCAG  
GACTCTGAATTCTAACATGCCAGTGACTGTCGCACTTGAGTTGAGGGCCAGTGGCCTG  
ATGAACGCTCACACCCCTCAGCTTAGAGTCTGCATTGGCTGTGACGCTCTCACCTGCC  
CAATAGATCTGCTCTGCTGCGACACCAGATCCACGTGGGACTCCCTGAGGCCCTGCTAAC  
TCCAGGCCTGGTCAGGTGACATTGCAGGATAAGCCAGGACCGGCACAGAAAGTGG  
TTGCCCTTNCCATTGCCCTCCCTGGNCATGCCCTTGCCTTGGAAAAAAATGATGAAGA  
AAACCTGGCTCTCCTTGCTGGAAAGGGTACTTGCTATGGGTTCTGGTGGCTAGAGA  
GAAAAGTAGAAAACCAGAGTCACGTAGGTGCTAACACAGAGGAGAGTAGGAACAGGGCGG  
ATACCTGAAGGTGACTCCGAGTCCAGGCCCTGGAGAAGGGTGGGGGGTGGTAAAGTA  
GCACAACACTATTTTTTCTTTCCATTATTATTGTTTTAAAGACAGAACCTCGTGC  
GCTGCCAGGCTGGAGTGCAGTGGCACGATCTGCAAACCTCCGCTCTGGGTTCAAGTGATT  
CTTCTGCCCTCAGCCTCCCGAGTAGCTGGGATTACAGGCACGCACCACACCTGGCTAATT  
TTTGTACTTTAGTAGAGATGGGTTTCACCATGTTGGCCAGGCTGGTCTGAACTCTGAC  
CTCAAATGAGCCTCTGCTCAGTCTCCAAATTGCCGGATTACAGGCATGAGCCACTGTG  
TCTGGCCCTATTCCCTTAAAAGTGAATTAAAGAGTTGTTCAAGTGCAGTATGCAAACCTGGAAAG  
ATGGAGGAGAAAAGAAAAGGAAGAAAAAAATGTCACCCATAGTCTCACCAAGAGACTATCAT  
TATTCGTTTGTTGACTTCCACTCTTCTTCACTACATAATTGCCGGTGTCTT  
TTTACAGAGCAATTATCTGTATATAACACTTGTATCCTGCCCTTACCTTATCGTCC  
ATCACTTTATTCCAGCACTCTGTGTTACAGACCTTTATAAATAAAATGTTCATCA  
GCTGCATAAAAAAAAAAAAAAA

## FIGURE 79

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44196
<subunit 1 of 1, 332 aa, 1 stop
<MW: 36143, pI: 5.89, NX(S/T): 1
MRLLVLLWGCLLPGYEALEGPEEISGFEGDTVSLQCTYREELRDHRKYWCRKGGILFSRCS
GTIYAAEEEGQETMKGRVSIRDLSRQELSLIVTLWNLTQDAGEYWCVEKRGPDESLLISLFV
FPGPCCPPSPSPTFQPLATTRLQPKAKAQQTQPPGLTSPGLYPAATTAKQGKTGAEAPPLPG
TSQYGHERTSQYTGTSPHPATSPAGSSRPPMQLDSTAEDTSPALSSGSSKPRVSIPMVRI
LAPVLVLLSLLSAAGLIAFCSHLLLWRKEAQQATETQRNEKFWLRLTAEEKEAPSQAPEGD
VISMPPLHTSEEELGFSKFVSA
```

**Important features:**

**Signal peptide:**

amino acids 1-17

**Transmembrane domain:**

amino acids 248-269

**N-glycosylation site.**

amino acids 96-99

**Fibrinogen beta and gamma chains C-terminal domain.**

amino acids 104-113

**Ig like V-type domain:**

amino acids 13-128

## FIGURE 80

TTGTGACTAAAAGCTGGCCTAGCAGGCCAGGGAGTGCAGCTGCAGCGTGGGGTGGCAGGA  
GCCGCAGAGCCAGAGCAGACAGCCGAGAACAGGTGGACAGTGTAAAGAACCAAGTGGTCTC  
GCTCTGTTGCCAGGCTAGAGTGTACTGGCGTGTACATAGCTCACTGCAGCCTCAGACTCCT  
GGACTTGAGAAATCCTCCTGCCTTAGCCTCCTGCATATCTGGGACTCCAGGGTGCACCAA  
GCCCTGTTCTCCTCTGTGAGTGGACCACGGAGGCTGGTGGCTGCAGCTGCCTGTCACTCCAA  
AGCTCAGCTCTGAGCCAGAGTGGTGGCTCCACCTCTGCCGCCGCATAGAACCCAGGAG  
CAGGGCTCTCAGAAGCGGTGGTGCCTCAGCTGGGATCATGTTGTTGGCCCTGGTCTGTCTGC  
TCAGCTGCCTGCTACCCCTCCAGTGAGGCCAAGCTCTACGGCGTTGTGAACTGGCCAGAGTG  
CTACATGACTTCGGGCTGGACGGATA~~CCGGGATA~~CAGCCTGGCTGACTGGGTCTGCCTTGC  
TTATTCACAAGCGGTTCAACGCAGCTGCTTGGACTACGAGGCTGATGGGAGCACCAACA  
ACGGGATCTCCAGATCAACAGCCGGAGGTGGTGCAGCAACCTCACCCGAACGTCCCCAAC  
GTGTGCCGGATGTACTGCTCAGATTGTTGAATCCTAATCTCAAGGATA~~CCGTTATCTGTGC~~  
CATGAAGATAACCCAAGAGCCTCAGGGCTGGGTTACTGGGAGGCCTGGAGGCATCACTGCC  
AGGGAAAAGACCTCACTGAATGGGTGGATGGCTGTGACTTCTAGGATGGACGGAACCATGCA  
CAGCAGGCTGGAAATGTGGTTGGTCCTGACCTAGGCTGGAAAGACAAGCCAGCGAATA  
AAGGATGGTTGAACGTGAAA

## FIGURE 81

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52187
<subunit 1 of 1, 146 aa, 1 stop
<MW: 16430, pI: 5.05, NX(S/T): 1
MLLALVCLLSCLLPSEAKLYGRCELARVLHDFGLDGYRGYSLADWVCLAYFTSGFNAAALD
YEADGSTNNNGIFQINSRRWCSNLTPNVPNVCRMYSQDILLNPNLKDTVICAMKITQEPMQGLGY
WEAWRHHCQGKDLTEWVDGCDF
```

**Important features:**

**Signal peptide:**

amino acids 1-18

**N-myristoylation site.**

amino acids 67-72

**Homologous region to Alpha-lactalbumin / lysozyme C proteins.**

amino acids 34-58 (catalytic domain), 111-132 and 66-107

## FIGURE 82

AGCCGCTGCCCGGGCGCCGCCGCGCGCACCAATGAGTCCCCGCTCGCCTGCGTTC  
GCTGCGCCTCCTCGTCTCGCCGTCTCTCAGCCGCCGAGCAACTGGCTGTACCTGGCCA  
AGCTGTCGTCGGTGGGAGCATCTCAGAGGAGGAGACGTGCAGAGAAACTCAAGGGCCTGATC  
CAGAGGCAGGTGCAGATGTGCAAGCGGAACCTGGAAGTCATGGACTCGGTGCGCCGCGTGC  
CCAGCTGGCCATTGAGGAGTGCCAGTACCAAGTTCCGGAACCGGGCGCTGGAACTGCTCCACAC  
TCGACTCCTGCCGTCTCGCAAGGTGGTGACGCAAGGGACTCGGGAGGCAGCCTCGTG  
TACGCCATCTCTCGGCAGGTGTGGCCTTGCAGTGACGCCGGCGTCAGCAGTGGGAGCT  
GGAGAAGTGCAGGCTGTGACAGGACAGTGCATGGGTCAAGCCCACAGGGCTTCCAGTGGTCAG  
GATGCTCTGACAACATCGCCTACGGTGTGGCCTCTCACAGTCGTTGTGGATGTGCGGGAG  
AGAAGCAAGGGGCCTCGTCCAGCAGGCCCTCATGAACCTCCACAACATGAGGCCGGCAG  
GAAGGCCATCCTGACACACATGCGGTGGAATGCAAGTGCCACGGGTGTCAGGCTCTGTG  
AGTAAAGACGTGCTGGCGAGCCGTGCCGCCCTCCGCCAGGTGGTCACGCACTGAAGGAG  
AAGTTGATGGTGCCACTGAGGTGGAGGCCACGCCGTGGCTCCTCCAGGGCACTGGTACC  
ACGCAACGCACAGTCAAGCCGACACAGATGAGGACCTGGTACTTGGAGCCTAGCCCCG  
ACTTCTGTGAGCAGGACATGCGCAGCGCGTGGCTGGCACGAGGGCCGCACATGCAACAAG  
ACGTCCAAGGCCATCGACGGCTGTGAGCTGCTGTGGCCGGCTTCCACACGGCGCA  
GGTGGAGCTGGCTGAACGCTGCAGCTGCAAATTCCACTGGTGTGCTTCGTCAAGTGCAGG  
AGTGCCAGCGGCTCGTGGAGTTGCACACGTGCCATGACCGCCTGCCTAGCCCTGCGCCGGC  
AACCACTAGTGGCCAGGGAAAGGCCATAATTAAACAGTCTCCCACCACTACCCAAGA  
GATACTGGTTGTATTTTGTGTTCTGGTTGGTTGGCTCATGTTATTTATTGCCGAA  
ACCAGGCAGGCAACCCCAAGGGCACCAACCAGGGCCTCCCCAAAGCCTGGGCTTGTGGCT  
GCCACTGACCAAAGGGACCTTGCTCGTGCCTGGCTGCCGATGTGGCTGCCACTGACCA  
CTCAGTTGTTATCTGTGTCCGTTCTACTTGAGACCTAAGGTGGAGTAACAAGGAGTAT  
TACCACCACATGGCTACTGACCGTGTATCGGGGAAGAGGGGGCCTATGGCAGGGAAAATA  
GGTACCGACTTGATGGAAGTCACACCCTCTGGAAAAAAAGAACTCTTAACTCTCCAGCACACA  
TACACATGGACTCCTGGCAGCTTGAGCCTAGAAGCCATGTCTCTCAAATGCCCTGAGAAAGG  
GAACAAGCAGATACCAAGGTCAAGGGACCAGGTTCAAGCCTACATGGACAGCTAGA  
GGTCGATATCTGTGGGTCTTCCAGGCAAGAAGAGGGAGATGAGAGCAAGAGACGACTGAA  
GTCCCACCCCTAGAACCCAGCCTGCCAGCCTGCCCTGGGAAGAGGAAACTTAACCACTCC  
CCAGACCCACCTAGGCAGGCATATAGGCTGCCATCCTGGACCAGGGATCCGGCTGTGCCTT  
TGCAGTCATGCCCGAGTCACCTTCACAGCGCTGTTCCATGAAAATGAAAAACACACAC  
AC  
GAGAGGGAGGAAAGGGCTGTGCCTTGCAGTCATGCCAGTCACCTTCACAGCACTGTTCTC

## **FIGURE 83**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48328
<subunit 1 of 1, 351 aa, 1 stop
<MW: 39052, pI: 8.97, NX(S/T): 2
MSPRSCLRSLLVFAVFSAAASNWLAKLSSVGSISEEETCEKLGLIQRQVQMCKRNLE
VMDSVRRGAQLAIEECQYQFRNRRWCNCSTLDSPVFGKVVTQGTREAAFVYAISSAGVAFAV
TRACSSGELEKCGCDRTVHGVPQGFQWSGCSDNIAYGVAFSQSFVDVRERSKGASSRALM
NLHNNEAGRKAILTHMRVECKCHGVSGSCEVKTCAVPPFRQVGHALKEKFDGATEVEPRR
VGSSRALVPRNAQFKPHTDEDLVYLEPSPDFCEQDMRSGVLGTRGRTCNKTSKAIDGCELLC
CGRGFHTAQVELAERCSCFKHWCCFVKCRQCQRLVELHTCR
```

**Important features:**

**Signal peptide:**

amino acids 1-22

**N-glycosylation sites.**

amino acids 88-91 and 297-300

**Wnt-1 family signature.**

amino acids 206-215

**Homologous region to Wnt-1 family proteins**

amino acids 183-235, 305-350, 97-138, 53-92 and 150 -174

## FIGURE 84

CGGACGCGTGGCGGACGCGTGGCGGACGCGTGGCGGACGCGTGGCTGGGTGCCTGCAT  
**CGCCATGG**AACCAACCAGGTACAGCAAGTGGGGCGCAGCTCCGAGGAGGTCCCCGGAGGGC  
CCTGGGGACGCTGGGTGCACTGGAGCAGGAGACCCCTCTTGCCTGGCTGTCCCTGGTC  
ACCACAGTCCTTGCGTGTGATTCTGAGTATCCTATTGTCCAAGGCCTCACGGAGCGC  
GGCGCTGCTTGACGCCACGACCTGCTGAGGACAACGCCCTCGAAGCAGACGGCGCGCTGG  
GTGCCCTGAAGGAGGAGGTGGAGACTGCCACAGCTGCTGCTGGGGACGCAGGCGCAGCTG  
CAGACCACGCCGCGCGAGCTGGGAGGCGCAGGCGAAGCTGATGGAGCAGGAGAGCGCC  
GCGGGAACTGCGTGAGCGCGTGACCCAGGGCTGGCTGAAGCCGGCAGGGCGTGAGGACG  
TCCGCACTGAGCTGTTCCGGCGCTGGAGGCCGTGAGGCTCCAGAACAACTCCTGCGAGCC  
TGCCCCACGTCGTGGCTGTCCTCGAGGGCTCTGCTACTTTCTCTGTGCCAAAGACGAC  
GTGGGCGGGCGCGCAGGATCACTGCGCAGATGCCAGCGCGCACCTGGTATCGTTGGGGCC  
TGGATGAGCAGGGCTTCCTCACTCGAACACCGCGTGGCGTGTTACTGGCTGGGCGTGAGG  
GCTGTGCCATCTGGCAAGGTTAGGGCTACCACTGGGTGGACGGAGTCTCTCAGCTT  
CAGCCACTGGAACCAGGGAGAGCCAATGACGCTGGGGCGCGAGAACACTGTGTATGATGC  
TGCACACGGGCTGGAACGACGCACCGTGTGACAGCGAGAACGGACGGCTGGATCTGTGAG  
AAAAGGCACAACTGCTGACCCCGCCAGTGCCCTGGAGGCCGCCATTGCAGCATGTC  
TCCTGGGGCTGTCACCTCCCTGGCTCCTGGAGCTGATTGCCAAAGAGTTTTCTTC  
CATCCACCGCTGCTGAGTCTCAGAACACTTGGCCAACATAGCCCTGTCCAGCCCAGTGC  
TGGGCTCTGGACCTCCATGCCGACCTCATCCTAACTCCACTCACGCAGACCCAACCTAAC  
TCCACTAGCTCCAAAATCCCTGCTCCTGCGTCCCCGTGATATGCCCTCACTCTCC  
CCAAGGTTAGGTGACTGAGGACTGGAGCTGTTGGTTCTCGCATTTCACCAA  
AGCTGTTTGCAAGCCTGAGGAAGCATCAATAAATATTGAGAAATGAAAAAA

## **FIGURE 85**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56352
<subunit 1 of 1, 293 aa, 1 stop
<MW: 32562, pI: 6.53, NX(S/T): 2
MDTTRYSKWGGSEEVPGGPWGRWVHWSRRPLFLALAVLVTTVLWAVILSILLSKASTERAA
LLDGHDLLRTNASKQTAALGALKEEVGDCHSCCSGTQAQLQTTRAELGEAQAKLMEQESALR
ELRERVTQGLAEAGRGRGREDVRTELFRALEAVRLQNNSCPCPTSWLSFEGSCYFFSVPKTTW
AAAQDHCADASAHLVIVGGLDEQGFLTRNTRGRGYWLGLRAVRHLGKVQGYQWVDGVSLFS
HWNQGEPNDAWGRENCVMMMLHTGLWNDAPCDSEKDGWICEKRHNC
```

**Important features:**

**Type II transmembrane domain:**

amino acids 31-54

**N-glycosylation sites.**

amino acids 73-76 and 159-162

**Leucine zipper pattern.**

amino acids 102-123

**N-myristoylation sites.**

amino acids 18-23, 133-138 and 242-247

**C-type lectin domain signature.**

amino acids 264-287

## FIGURE 86

GCCAGGGGAAGAGGGT GATCCGACCCGGGAAGGT CGCTGGCAGGGCGAGTTGGGAAAGCG  
GCAGCCCCGCCGCCCG CAGCCCCTCTCCTCTTCTCCCACGT CCTATCTGCCTCTCG  
CTGGAGGCCAGGCCGT GCAGCATCGAAGACAGGAGGA ACTGGAGCCTCATGGCCGGCCGG  
GGCGCCGGCCTCGGGCT TAAATAGGAGCTCCGGCTCTGGCTGGGACCCGACCGCTGCCGGC  
CGCGCTCCCGCTGCTCCTGCCGGTG **ATGGAAAACCCCAGCCGGCCGCCCTGGCAAG**  
GCCCTCTGCCTCTCCTGCCACTCTCGCGCCGCCAGCCTCTGGGGAGAGTC  
CATCTGTTCCGCCAGAGCCCCGCCAAATACAGCATCACCTCACGGGCAAGTGGAGCCAGA  
CGGCCTTCCCCAAGCAGTACCCCTGTTCCGCCCGCGCAGTGGCTTCGCTGGGG  
GCCGCGCATAGCTCCGACTACAGCATGTGGAGGAAGAACAGTACGT CAGTAACGGGCTGCG  
CGACTTTGCGGAGCGCGCGAGGCCCTGGCGCTGATGAAGGAGATCGAGGCCGGGGAGG  
CGCTGCAGAGCGTGCACGAGGTGTTTCCGCCGCCGTCCCCAGCGGACCGGGCAGACG  
TCGGCGAGCTGGAGGTGCAGCGCAGGCACTCGCTGGTCTCGTTGTGGTGCATCGTGC  
CAGCCCCACTGGTCTGGACCTGTACCCCTACGACGCCGGACGGACAGCGGCTTCACCTTCTCC  
TCCCCCAACTCGCCACCATCCGCAGGACACGGTACCGAGATAACGTCTCCTCTCCAG  
CCACCCGGCCA ACTCCTCTACTACCCCGGCTGAAGGCCCTGCCCTCCATGCCAGGGTGA  
CACTGCTGCGGCTGCGACAGAGCCCCAGGGCTTCATCCCTCCGCCAGTCCTGCCAGC  
AGGGACAATGAGATTGTAGACAGCGCCTCAGTCCAGAAACGCCGCTGGACTGCGAGGTCTC  
CCTGTGGTGTCTGGGACTGTGCGGAGGCCACTGTGGGAGGCTGGACCAAGAGCAGGA  
CTCGCTACGTCCGGTCCAGCCGCAACAACGGGAGCCCCTGCCCGAGCTCGAAGAAGAG  
GCTGAGTGCCTGCTGATAACTGCGT **CTAAG** ACCAGAGCCCCG CAGCCCTGGGGCCCCCG  
GAGCCATGGGTGTCGGGGCTCTGTGCAGGCTCATGCTGCAGGCCGGAGGGCACAGGG  
GGTTTGCCTGCTCCTGACCGCGGTGAGGCCGCCGACCATCTCTGCACTGAAGGCCCT  
CTGGTGGCCGGCACGGCATTGGAAACAGCCTCCTCCCTTCCAACCTTGCTTAGGGG  
CCCCCGTGTCCGTCTGCTCTCAGCCTCCTCCTGCAGGATAAAGTCATCCCCAAGGCTC  
CAGCTACTCTAAATTATGTCTCCTTATAAGTTATTGCTGCTCCAGGAGATGTCCTTCATCG  
TCCAGGGGCTGGCTCCCACGTGGTGCAGATAACCTCAGACCTGGTGCCTAGGCTGTGCTG  
AGCCCACCTCCCGAGGGCGCATCCAAGCGGGGCCACTTGAGAAGTGAATAATGGGGCGG  
TTTCGGAAGCGTCAGTGTCCATGTTATGGATCTCTCGCTTGAAATAAGACTATCTCT  
GTTGCTCACAAAAAAAAAAAAAAA

## FIGURE 87

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53971
><subunit 1 of 1, 331 aa, 1 stop
><MW: 35844, pi: 5.45, NX(S/T): 2
MENPSPAAALGKALCALLLATLGAAGQPLGGESICSARAPAKYSITFTGKWSQTAFPKQYPL
FRPPAQWSLLGAAHSSDYSMWRKNQYVSNGLRDFAERGEAWALMKEIEAAGEALQSVHEVF
SAPAVPSGTGQTSAELEVQRHSLVSFVVRIVPSPDWFVGVDSDLLCDGDRWREQAALDLYP
YDAGTDSGFTFSSPNFATIPQDTVTEITSSSPSHPANSFYYPRLKALPPIARVTLLRLRQSP
RAFIIPPAPVLPSPRDNEIVDSASVPETPLDCEVSLWSSWGLCGGHCGRLGTSRTRYVRVQPA
NNGSPCPELEEEAECVPDNCV
```

**Important features:**

**Signal peptide:**

amino acids 1-26

## **FIGURE 88**

GGCGGCGTCCGTGAGGGCTCTTGGCAGGGTAGTGTGTTGGTGTCCCTGTCTGCGTGA  
TATTGACAAACTGAAGCTTCCTGCACCACTGGACTTAAGGAAGAGTGACTCGTAGGCGGA  
CAGCTTAGTGGCCGGCCGGCGCTCATCCCCGTAAGGAGCAGAGTCCTTGTACTGAC  
**CAAGATGAGCAACATCTACATCCAGGAGCCTCCCACGAATGGAAAGGTTTATTGAAA**ACTA  
CAGCTGGAGATATTGACATAGAGTTGGTCAAAGAACGCTCTAAAGCTTGCAGAAATT  
ATCCAACTTGTTGGAAGCTTATTATGACAATACCATTTTACAGAGTTGTGCCTGGTTT  
CATAGTCCAAGGCGGAGATCCTACTGGCACAGGGAGTGGTGGAGAGTCTATCTATGGAGCGC  
CATTCAAAGATGAATTCATTACGGTTGCGTTTAATCGGAGAGGACTGGTGCATGGCA  
AATGCTGGTCTCATGATAATGGCAGCCAGTTTCTCACACTGGTCGAGCAGATGAAC  
TAACAATAAGCATAACCCTTGGAAAGGTTACAGGGATACAGTATATAACATGTTGCGAC  
TGTCAAGTAGACATTGATGATGACGAAAGACCACATAATCCACACAAAATAAAAGCTGT  
GAGGTTTGTAAATCCTTTGATGACATCATTCAAGGGAAATTAAAAGGCTGAAAAAAGA  
GAAACCAGAGGAGGAAGTAAAGAAATTGAAACCCAAAGGCACAAAAAATTAGTTACTTT  
CATTGGAGAGGAAGCTGAGGAAGAAGAGGGAGGAAGTAAATCGAGTTAGTCAGAGCATGAAG  
GGCAAAAGCAAAAGTAGTCATGACTTGCTTAAGGATGATCCACATCTCAGTTCTGTTCCAGT  
TGTAGAAAGTGAAAAGGTGATGCACCAGATTAGTTGATGATGGAGAAGATGAAAGTGCAG  
AGCATGATGAATATATTGATGGTGATGAAAAGAACCTGATGAGAGAAAGAATTGCCAAAAAA  
TTAAAAAAAGGACACAGTGCATGCAATGTTAAATCAGCTGGAGAAGGAGAAGTGGAGAAGAAATC  
AGTCAGCCGCAGTGAAGAGCTCAGAAAAGCAAGACAATTAAAACGGAACTTTAGCAG  
CAAAACAAAAAAAGTAGAAAATGCAGCAAAACAAGCAGAAAAAGAAGTGAAGAGGAAGAA  
GCCCTCCAGATGGTGTGCGAATACAGAAGAGAAAAGCAAAAGTATGAAGCTTGAG  
GAAGCAACAGTCAGGAAACTTCCGGAGATCAGACCCCTGCACTGCTGAACCAAGT  
TTAAATCTAAACTCACTCAAGCAATTGCTGAAACACCTGAAATGACATTCTGAAACAGAA  
GTAGAAGATGATGAAGGATGGATGTACATGACTTCAGTTGAGGATAAAAGCAGAAAAGT  
GAAAGATGCAAGCATGCAAGACTCAGATACTTGAATCTATGATCCTCGGAATCCAGTGA  
ATAAAAGAAGGAGGAAGAAGCAAAAGCTGATGAGAGAGAAAAAGAAAGAAGATAAAAT  
GAGAATAATGATAACCAGAACTTGCTGGAAATGTGCCTACAATGGCCTGTAACAGCCATTG  
TTCCCAACAGCATCACTTAGGGGTGTGAAAAGAAGTATTGAAACCTGTTGTCTGGTTT  
AAAAACAATTATCTGTTGCAAATTGGAATGATGTAAGCAAATGCTTTGGTTACTGG  
TACATGTGTTTCTAGCTGACCTTATATTGCTAAATCTGAAATAACTTCCCT  
TCCACAAAAAA

## **FIGURE 89**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50919
><subunit 1 of 1, 472 aa, 1 stop
><MW: 53847, pI: 5.75, NX(S/T): 2
MSNIYIQEPPTNGVLLKTTAGDIDIELWSKEAPKACRNFIQLCLEAYYDNTIFHRVVPGFI
VQGGDPTGTGSGGESIYGAPPFKDEFHSRLRFNRRGLVAMANAGSHDNGSQFFTLGRADELN
NKHTIFGKVTGDTVYNMLRLSEVDIDDDERPHNPKIKSCEVLFNPFDIIPREIKRLKKEK
PEEEVKKLKPKGTKNFSLLSFGEAAEEEEEVNRVSQSMKGKSKSSHDLKDDPHLSSVPVV
ESEKGDAPDLVDDGEDESAEHDEYIDGDEKNLMRERIAKKLKDDTSANVKSAGEGEVEKKSV
SRSEELRKEARQLKRELLAAKQKKVENAAKQAEKRSEEEEAPPDGAVAAYRREKQKYEALRK
QQSKKGTSREDQTLALLNQFKSKLTQAIATPENDIPETEVEDDEGWMHSVLFEDKSRKVK
DASMQDSDTFEIYDPRNPVNRRREESKLMREKKERR
```

**Important features:**

**Signal peptide:**

amino acids 1-21

**N-glycosylation sites.**

amino acids 109-112 and 201-204

**Cyclophilin-type peptidyl-prolyl cis-trans isomerase signature.**

amino acids 49-66

**Homologous region to Cyclophilin-type peptidyl-prolyl cis-trans isomerase**

amino acids 96-140, 49-89 and 22-51

## **FIGURE 90**

CGCCGCCGTTGGGGCTGGAAGTTCCCAGGTCCGTGCCGGGAGAGAGATGCTGCCGG  
CCGCCTCGGCTTGAGGCAGAGAAGTGTCCCAGACCCATTGCGCTGCTGACGGCGTCG  
AGCCCTGGCAGACATGTCCACAGGGTTCTCCTCGGGACTCTGGCTCCACCACC  
GTGGCCGCCGGCGGGACCAGCACAGGGCGTTCTCCTCGGAACGGAACGTCTAGCAA  
CCCTCTGTGGGGCTCAATTGGAAATCTTGAAGTACTTCAACTCCAGCAACTACATCTG  
CTCCTCAAGTGGTTTGAACCGGGCTTTGGATCTAAACCTGCCACTGGTTCACTCTA  
GGAGGAACAAATACAGGTGCTTGACACCAAGAGGCCCAAGTGGTACCAAATATGGAAC  
CCTGCAAGGAAAACAGATGCATGTGGGAAGACACCCATCCAAGTCTTTAGGAGTCCCCT  
TCTCCAGACCTCCTAGGTATCCTCAGGTTGCACCTCCAGAACCCCCGGAGCCCTGGAAA  
GGAATCAGAGATGCTACCACCTACCCGCTGGATGGAGTCTCGCTCTGCGCAGGCTGGAG  
TGCAGTGGCACGATCTCGGCTCACTGCAACCTCCGCCTCCGGTTCAAGCGAGTCTCCTGC  
CTCAGCCTCTGAGTGTCTGGGGCTACAGGTGCTGCAGGAGTCCTGGGCCAGCTGGCCTCG  
ATGTACGTCAGCACGCCGGAACGGTACAAGTGGCTGCCTCAGCGAGGACTGTCTGTACCT  
GAACGTGTACGCGCCGGCGCCGGGATCCCCAGCTGCCAGTGTGGCTGGTTCC  
CGGGAGGCCCTCATCGTGGCGCTGCTTCTCGTACGACAGGCTGGCATCTCGGCTTCTGAGCACGGA  
GAGAAAGTGGTGTGGTTCTGAGCACAGGCTGGCATCTCGGCTTCTGAGCACGGA  
CGACAGCCACGCGCCGGAACTGGGGCTGCTGGACCAGATGGCGCTTGTGGCTGGTGC  
AGGAGAACATCGCAGCCTCGGGGAGACCCAGGAAATGTGACCCTGTTGGCCAGTCGGCG  
GGGGCCATGAGCATCTCAGGACTGATGATGTCACCCCTAGCCTGGGTCTCTCCATGGGC  
CATTCCCAGAGTGGCACCGCGTTATTCAAGACTTTCATCACTAGTAACCCACTGAAAGTGG  
CCAAGAACGTTGCCACCTGGCTGGATGCAACCACAACAGCACAGATCCTGGTAAACTGC  
CTGAGGGCACTATCAGGGACCAAGGTGATGCGTGTCCAACAAGATGAGATTCTCCACT  
GAACCTCCAGAGAGACCCGGAAGAGATTATCTGGTCCATGAGCCCTGTGGTGGATGGTGTGG  
TGATCCCAGATGACCCATTGGTGTCTGACCCAGGGGAAGGTTCATCTGTGCCCTACCTT  
CTAGGTGTCAACAAACCTGGAATTCAATTGGCTTGTGCTTATAATATCACCAAGGAGCAGGT  
ACCACTTGTGGAGGAGTACCTGGACAATGTCAATGAGCATGACTGGAAGATGCTACGAA  
ACCGTATGATGGACATAGTTCAAGATGCCACTTCGTGTATGCCACACTGCAGACTGCTCAC  
TACCACCGAGAAACCCAATGATGGAAATCTGCCCTGCTGGCCACGCTACAACAAGGATGAA  
AAGTACCTGCAGCTGGATTAACTACACAGAGTGGCATGAAGCTCAAGGAGAAGAACGATGGC  
TTTTGGATGAGTGTACCAGTCTCAAAGACCTGAGAAGCAGAGGCAATTCTAAGGGTGGC  
TATGCAGGAAGGAGCCAAAGAGGGTTGCCCTACCATCCAGGCCCTGGGAGACTAGCCA  
TGGACATACCTGGGACAAGAGTTCTACCCACCCAGTTAGAACTGCGAGGAGTCCTGCT  
GCCTCCAGGCCAAAGCTAGAGCTTGTGCTGTGGACCTGCACTGCCCTTCCAGCC  
TGACATCCCATGATGCCCTACTTCAGTGTGACATCCAGTTAGGCCAGGCCCTGTCAAC  
ACCACACTGTGCTCAGCTCCAGCCTCAGGACAACCTTTTCTTCAATCCT  
CCCACCCCTCAATGTCTCTGTGACTCCTCTTATGGGAGGTGACCCAGACTGCCACTGC  
CCCTGTCAGTGCACCCAGCTGGCATTACCATCCACTCTGCTCAACCTGTTCTGTCTGT  
TCACATTGGCCTGGAGGCCTAGGGCAGGTTGTGACATGGAGCAAACCTTGGTAGTTGGGA  
TCTCTCTCCCACCCACACTTATCTCCCCAGGGCACTCCAAAGTCTATACACAGGGTGG  
TCTCTCAATAAGAAGTGTGATTAGAAAAAAAAAAAAA

## FIGURE 91

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44179
<subunit 1 of 1, 545 aa, 1 stop
<MW: 58934, pI: 9.45, NX(S/T): 4
MSTGFSFGSGTTLGTTVAAGGTSTGGVFSFGTGTSSNPSVGLNFGNLGSTSTPATT SAPSSG
FGTGLFGSKPATGFTLGGTNTGALHTKRPQVVTKYGTLQGKQMHVGKTPIQVFLGVPPSRPP
LGILRFAPPEPPEPKGIRDATTYPPGWSLALSPGWSAVARSRLTATSASRVQASLLPQPLS
VWGYRCLQESWGQLASMYVSTRERYKWLRFSEDCLYLNVYAPARAPGDPQLPVMVWFPGGAF
IVGAASSYEGSDLAAREKVVLVFLQHRLGIFGFLSTDDSHARGNWGLLDQMAALRWVQENIA
AFGGDPGNVTLFGQSAGAMSISGLMMSPLASGLFHRAISQSGTALFRLFITSNPLKVAKKVA
HLAGCNHNSTQILVNCLRALS GTKVMRVSNKMRFLQLNFQRDPEEIIWSMSPVVDGVVI PDD
PLVLLTQGVSSVPYLLGVNNLEFNWLLPYNITKEQVPLVVEYLDNVNEHDWKMLRNRMMD
IVQDATFVYATLQTAHYHRETPMMGICPAGHATTRMKSTCSWILPQEWA
```

**Important features:**

**Signal peptide:**

amino acids 1-29

**Carboxylesterases type-B serine active site.**

amino acids 312-327

**Carboxylesterases type-B signature 2.**

amino acids 218-228

**N-glycosylation sites.**

amino acids 318-321, 380-383 and 465-468

## FIGURE 92

GAGAACAGGCCTGTCAGGCAGGCCCTGCGCCTCCTATGCGGAGATGCTACTGCCACTGCT  
GCTGTCCCTCGCTGCTGGCGGGTCCCAGGCTATGGATGGGAGATTCTGGATACGAGTGCAGG  
AGTCAGTGATGGTGCCGGAGGGCCTGTGCATCTCTGTGCCCTGCTCTTCTCCTACCCCCGA  
CAAGACTGGACAGGGTCTACCCCAGCTTATGGCTACTGGTTCAAAGCAGTGACTGAGACAAC  
CAAGGGTGCCTCTGTGGCCACAAACCACCAAGAGTCGAGAGGTGAAATGAGCACCCGGGGCC  
GATTCCAGCTCACTGGGGATCCGCCAAGGGAACTGCTCCTGGTGTAGAGACGCGCAG  
ATGCAGGATGAGTCACAGTACCTCTTCGGGTGGAGAGAGGAAGCTATGTGACATATAATT  
CATGAACGATGGGTTCTTCTAAAAGTAACAGTGCTCAGCTCACGCCAGACCCAGGACC  
ACAACACCGACCTCACCTGCCATGTGACTTCTCCAGAAAGGGTGTGAGCGCACAGAGGACC  
GTCCGACTCCGTGTGGCCTATGCCCCAGAGACCTTGTATCAGCATTACGTGACAACAC  
GCCAGCCCTGGAGCCCCAGCCCCAGGGAAATGTCCCATACTGGAAGCCCCAAAAGGCCAGT  
TCCTGCGGCTCCTCTGTGCTGACAGCCAGCCCCCTGCCACACTGAGCTGGTCTGCAG  
AACAGAGTCTCTCTCGTCCCACCTGGGGCCCTAGACCCCTGGGCTGGAGCTGCCGG  
GGTGAAGGCTGGGATTCAAGGGCCTACACCTGCCAGCGGAGAACAGGCTGGCTCCAGC  
AGCGAGCCCTGGACCTCTGTGCACTATCCTCCAGAGAACCTGAGAGTGATGGTTCCCAA  
GCAAACAGGACAGTCCTGGAAAACCTGGAACGGCACGTCTCCAGTACTGGAGGGCCA  
AAGCCTGTGCCTGGTCTGTGTCACACACAGCAGCCCCCAGCCAGGCTGAGCTGGACCCAGA  
GGGGACAGGTTCTGAGCCCCCTCCAGCCCTCAGACCCCCGGGTCTGGAGCTGCCTGGGTT  
CAAGTGGAGCACGAAGGAGAGTTCACCTGCCACGCTGGCACCCACTGGGCTCCCAGCACGT  
CTCTCTCAGCCTCTCGTGCACTATAAGAAGGGACTCATCTCAACGGCATTCTCCAACGGAG  
CGTTTCTGGGAATCGGATCACGGCTCTTCTTCTCGCCTGCCCTGATCATCATGAAG  
ATTCTACCGAAGAGACGGACTCAGACAGAAACCCCGAGGGCCAGGGTTCTCCCGGCACAGCAC  
GATCCTGGATTACATCAATGTGGTCCCGACGGCTGGCCCCCTGGCTCAGAAGCGGAATCAGA  
AAGCCACACCAACAGTCCTCGGACCCCTCTCCACCAAGGTGCTCCCTCCCCAGAATCAAAG  
AAGAACCAAGAAAAAGCAGTATCAGTTGCCAGTTCCAGAACCCAAATCATCCACTCAAGC  
CCCAGAATCCCAGGAGAGCCAAGAGGAGCTCCATTATGCCACGCTCAACTCCAGGCGTCA  
GACCCAGGCCTGAGGCCCGGATGCCAAGGGCACCCAGGCGATTATGCAGAAGTCAAGTTC  
CAATGAGGGCTCTTAGGCTTAGGACTGGACTTCCGCTAGGGAGGAAGGTAGAGTAAGAG  
GTTGAAGATAACAGAGTGCAAAGTTCTCTCTCCCTCTCTCTCTCTCTCTCTCTCTCT  
CTCTCTTCTCTCTCTTTAAAAAACATCTGCCAGGGCACAGTGGCTCACGCCTGTAATC  
CCAGCACTTGGGAGGTTGAGGTGGCAGATGCCCTGAGGTGGAGTTCGAGACCAGCCTG  
GCCAACTTGGTAAACCCGCTCTACTAAAAATACAAAAATTAGCTGGCATGGTGGCAGG  
CGCCTGTAATCCTACCTACTTGGGAAGCTGAGGCAGGAGAACACTTGAACCTGGGAGACGG  
AGGTTGCAGTGAGCCAAGATCACACCAATTGCACGCCAGCCTGGCAACAAAGCGAGACTCCA  
TCTAAAAAAAAATCCTCAAATGGTTGGTGTGTAATCCCAGCACTTGGGAGGCTA  
AGGTGGGTGGATTGCTTGAGGCCAGGAGTTGAGACCAAGCCTGGCAACATGGTAAACCC  
ATCTCTACAAAAATACAAAACATAGCTGGCTTGGTGTGTCCTGTAAGTCCAGCTGT  
CAGACATTAAACCAAGAGCAACTCCATCTGGAAATAGGAGCTGAATAAAATGAGGCTGAGACC  
TACTGGCTGCATTCTCAGACAGTGGAGGCATTCTAAGTCACAGGATGAGACAGGAGGTCCG  
TACAAGATAACAGGTATAAAGACTTGTGATAAAAACAGATTGCAAGTAAAGAAGCCAACCAA  
ATCCCCACCAAAACCAAGTTGCCACGAGAGTGACCTCTGGTGTGTCCTCACTGCTACACTCCT  
GACAGCACCATGACAGTTACAAATGCCATGGCAACATCAGGAAGTTACCCGATATGTCCCA  
AAAGGGGGAGGAATGAATAATCCACCCCTGTTAGCAAATAAGCAAGAAATAACCATAAAA  
GTGGGCAACCAGCAGCTAGGCCTGCTTGTATGGAGTAGCCATTCTTTGTTCCCTT  
TACTTCTTAATAAACTTGCTTACCTTAAAAAA

## FIGURE 93

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA54002  
><subunit 1 of 1, 544 aa, 1 stop  
><MW: 60268, pI: 9.53, NX(S/T): 3  
MLLPLLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWGSTPAYGYWFK  
AVTETTKGAPVATNHQSREVERMSTRGRFQLTGDPAKGNCSLVIRDAQMDESQYFFRVERGS  
YVTYNFMNDGFFLKVTVL SFTPQDHN DLTCHVDFSRKGVSAQRTVRLRVAYAPRDLVIS  
ISRDNTPALEPQPQGNVPYLEAQKGQFLRLCAADSQPPATLSWVLQRNLSSHPWGPRPL  
GLELPGVKAGDSGRYTCRAENRLGSQQRALDLSVQYPHENLRVMVSQANRTVLENLGNGTSL  
PVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHEGEFTCHARHP  
LGSQHVSLSLSVHYKKGLISTAFSNGAFLGIGITALLFLCLALIIMKILPKRRTQTETPRPR  
FSRHSTILDYINVVPTAGPLAQKRNQKATPNSPRTPPPAGAPSPESKKNQKKQYQLPSFPEP  
KSSTQAPESQESQEELHYATLNFPGVRPRPEARMPKGTQADYAEVKFQ

**Important features:**

**Signal peptide:**

amino acids 1-15

**Transmembrane domain:**

amino acids 399-418

**N-glycosylation site.**

amino acids 100-103, 297-300 and 306-309

**Immunoglobulins and major histocompatibility complex proteins signature.**

amino acids 365-371

## **FIGURE 94**

TGAAGAGTAATAGTGGAAATCAAAAGAGTCACCGCAATGAACTGTTATTACTGCTGCGT  
TTA  
TATGTTGGAAATTCCCTCCTATGGCCTTGTCTGGAGCAACAGAAA  
ACTCTCAAACAAAGA  
AAAGTCAGCAGCCAGTGCATCTCATTGAGAGTGAAGCGTGGCTGGGTG  
GAACCAATT  
TTTGTACCAGAGGAATGAATACGACTAGTCATCACATCGGCCAGCTAAGATCTGATTAGA  
CAATGGAAACAATTCTTCCAGTACAAGCTTTGGGAGCTGGAGCTGGAAAGTACTTTATCA  
TTGATGAAAGAACAGGTGACATATATGCCATACAGAAGCTTGATAGAGAGGAGCGATCC  
CT  
TACATCTTAAGAGCCCAGGTAAAGACATCGCTACTGGAAGGGCTGTGGAAACCTGAGTCTGA  
GTTGTCATCAAAGTTCCGGATATCAATGACAATGAACCAAATTCTAGATGAACCTTATG  
AGGCCATTGTACCAGAGATGTCTCCAGAAGGAACATTAGTTATCCAGGTGACAGCAAGTGA  
GCTGACGATCCCTCAAGTGGTAATAATGCTCGTCTCTACAGCTTACTCAAGGCCAGCC  
ATATTTCTGTTGAACCAACAACAGGAGTCATAAGAATATCTCTAAAATGGATAGAGAAC  
TGCAAGATGAGTATTGGGTAATCATTCAAGCCAAGGACATGATTGGTCAGCCAGGAGCGTTG  
TCTGGAAACAACAAGTGTATTAATTAAACTTCAAGTGTAAATGACAATAAGCCTATATTAA  
AGAAAGTTTATACCGCTTGACTGTCTGAATCTGCACCCACTGGACTTCTATAGGAACAA  
TCATGGCATATGATAATGACATAGGAGAGAATGCAGAAATGGATTACAGCATTGAAGAGGAT  
GATTGCAAAACATTGACATTACTAATCATGAAACTCAAGAAGGAATAGTTATATTAA  
AAAGAAAGTGGATTGAGCACCAGAACACTACGGTATTAGAGCAAAAGTTAAAACCATC  
ATGTTCCCTGAGCAGCTCATGAAGTACCAACTGAGGCTTCCACCACTTCATTAAGATCCAG  
GTGGAAGATGTTGATGAGCCTCTTTCTCTCCATATTATGTATTGAAAGTTTG  
AGAAACCCACAGGGATCATTGTAGGCCTGGTCTGCCACAGACCCAGACAATAGGAAT  
CTCCTATCAGGTATTCTATTACTAGGAGCAAAGTGTCAATATCAATGATAATGGTACAATC  
ACTACAAGTAACTCACTGGATCGTAAATCAGTGTCTGGTACAACCTAAGTATTACAGCCAC  
AGAAAATACAATATAGAACAGATCTCTCGATCCACTGTATGTGCAAGTTCTTAACATCA  
ATGATCATGCTCCTGAGTTCTCAATACTATGAGACTATGTTGAAATGCAGGCTCT  
GGTCAGGTAACTCAGACTATCAGTGCAGTGGATAGAGATGAATCCATAGAACAGCACCATT  
TTACTTTAATCTATCTGTAGAAGACACTAACAAATTCAAGTTTACAATCATAGATAATCAAG  
ATAACACAGCTGTCTTGTACTAACAGAACTGGTTAACCTTCAAGAAGAACCTGTCTC  
TACATCTCCATCTTAATTGCCGACAATGGAATCCGTACTTACAAGTACAAACACCCCTAC  
CATCCATGTCTGTGACTGTGGTACAGTGGAGCACACAGACACTGCCAGTACCA  
GGAGCTTGCTTCAAGACAGAAAGTTATCATTGCTATTCTCATTTGATTGATCATA  
TTGGGTTATTTTGACTTGGGTTAAAACAACGGAGAAAACAGATTCTATTCTGA  
GAAAAGTGAAGATTCAAGAGAAATATATTCCAATATGATGATGAAGGGGTGGAGAACAG  
ATACAGAGGCCTTGATATAGCAGAGCTGAGGAGTAGTACCAATGCGGGAACGCAAGACT  
CGGAAAACCACAAGCGCTGAGATCAGGAGCCTACAGGCAGTCTTGCAGTTGGCCCCGA  
CAGTGCCTATTCAAGGAAATTCAATTCTGGAAAAGCTCGAAGAACGTAATAACTGATCC  
GTGCTTCTTGTGATTCCCTCAGACCTACGCTTTGAGGGAACAGGGTATTAGCTGGATCC  
CTGAGCTCCTTGAATCAGCAGTCTGATCAGGATGAAAGCTATGATTACCTTAATGAGTT  
GGGACCTCGCTTAAAAGATTAGCATGCATGTTGGTCTGCAGTGCAGTCAAATAATTAGG  
GCTTTTACCATCAAAATTAAAAGTCTAATGTGATTGCAACCCAATGGTAGTCTTAA  
AGAGTTTGTGCCCTGGCTCATGGGGGAAAGCCCTAGTCTATGGAGTTCTGATTCC  
CTGGAGTAAATACCTCATGGTATTTAAGCTACCTACATGCTGTCAATTGAAACAGAGATGTG  
GGGAGAAATGTAACAAATCAGCTCACAGGCATCAATACAACCAAGATTTGAAGTAAAATAATG  
TAGGAAGATATTAAAGTAGATGAGAGGACACAAGATGTAGTCGATCCTTATGCGATTATAT  
CATTATTACTAGGAAAGAGTAAAATACCAACGAGAAAATTAAAGGAGCAAAATTG  
CAAGTCAAATAGAAATGTACAAATCGAGATAACATTACATTCTATCATATTGACATGAAA  
ATTGAAAATGTATAGTCAGAGAAATTTCATGAATTATTCCATGAAGTATTGTTCTTAT  
TTAAA

## FIGURE 95

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53906
><subunit 1 of 1, 772 aa, 1 stop
><MW: 87002, pi: 4.64, NX(S/T): 8
MNCYLLLRFMLGIPPLLWPCLGATENSQTKVKQPVRSHLRVKRGWVWNQFFVPEEMNTTSHH
IGQLRSDLNDGNNSFQYKLLGAGAGSTFIIDERTGDIYAIQKLDREERSLYILRAQVIDIAT
GRAVEPESEFVIKVSDINDNEPKFLDEPYEAIPEMSPEGTLVIQVTASDADDPSSGNARL
LYSLLQGQPYFSVEPTTGVIARISSKMDRELQDEYWVIIQAKDMIGQPGALSGTTSVLIKLSD
VNDNKPIFKESLYRLTVSESAPGTTSIGTIMAYDNDIGENAEMDYSIEEDDSQTFDIITNHE
TQEGIVILKKKVDFEHQNHYGIRAKVKNHHVPEQLMKYHTEASTTFIKIQVEDVDEPPLFLL
PYYVFEVFEETPQGSFVGVVSATDPDNRKSPIRYSITRSKVFNINDNGTITTSNSLDREISA
WYNLSITATEKYNIEQISSIPLYVQVLNINDHAPEFSQYYETYVCENAGSGQVIQTISAVDR
DESIEHHFYFNLSVEDTNNSSFTIIDNQDNTAVILTNRGFLQEEPVFYISILIADNGIP
SLTSTNTLTIHVCDCGDGSQTQCQYQELVLSMGFKTEVIIAILICIMIIFGFIFLTLGLKQ
RRKQILFPEKSEDFRENIFQYDDEGGGEEDTEAFDIAELRSSTIMRERKTRKTTSAEIRSLY
RQSLQVGPDSAIFRKFILEKLEEANTDPCAPPFDLQTYAFEGTGSLAGSLSSLESAVSDQD
ESYDYLNELGPRFKRLACMFGSAVQSNN
```

**Important features:**

**Signal peptide:**

amino acids 1-21

**Transmembrane domain:**

amino acids 597-617

**N-glycosylation sites.**

amino acids 57-60, 74-77, 419-423, 437-440, 508-511, 515-518,  
516-519 and 534-537

**Cadherins extracellular repeated domain signature.**

amino acids 136-146 and 244-254

## **FIGURE 96**

ATTTCAAGGCCAGCCATATTTNTGTTGAACCAACAACAGGAGTCATAAGAATATTTNTA  
AAATGGATAGAGAACTGCAAGATGAGTATTGGGTAAATCATTCAAGCCAAGGACATGATTGGT  
CAGCCAGGAGCGTTGTNTGGAACAAACAAGTGTATTAATTAAACTTCAGATGTTAATGACAA  
TAAGCCTATATTTAAAGAAAGTTATACCGCTTGACTGTNTNTGAATCTGCACCCACTGGGA  
NTTNTATAGGAACAATCATGGCATATGATAATGACATAGGAGAGAATGCAGAAATGGATTAC  
AGCATTGAAGAGGATGATTGCAAACATTTGACATTATT

## **FIGURE 97**

GCAACCTCAGCTTCTAGTATCCAGACTCCAGCGCCGCCCCGGCGCGAACCCAACCCGAC  
CCAGAGCTTCTCCAGCGCGCGCAGCGAGCAGGGCTCCCGCCTTAACCTCCCTCCGCGGGG  
CCCAGCCACCTTCGGGAGTCGGGTTGCCACCTGCAAACCTCTCCGCTTCTGCACCTGCCA  
CCCCTGAGCCAGCGCGGGCCCCGAGCGAGTC**ATGG**CCAACGCAGGGCTGCAGCTGTTGGC  
TTCATTCTCGCCTCCTGGGATGGATCGGCGCCATCGTCAGCACTGCCCTGCCCACTGGAG  
GATTACTCCTATGCCGGCGACAACATCGTACCGCCCAGGCCATGTACGAGGGGCTGTGGA  
TGTCCCTGCGTGTGCGAGAGCACCGGGCAGATCCAGTCAAAGTCTTGACTCCTGCTGAAT  
CTGAGCAGCACATTGCAAGCAACCGTGCCTGATGGTGGTGGCATCCTCTGGAGTGAT  
AGCAATCTTGTGGCCACCCTGGCATGAAGTGTATGAAGTGCTTGAAGACGATGAGGTGC  
AGAAGATGAGGATGGCTGTCAATTGGGGTGCATATTCTTCTGCAGGTCTGGCTATTAA  
GTTGCCACAGCATGGTATGGAATAGAATCGTCAAGAATTCTATGACCCATGACCCAGT  
CAATGCCAGGTACGAATTGGTCAGGCCTCTTCACTGGCTGGGCTGCTGCTCTCTGCC  
TTCTGGGAGGTGCCCTACTTGCTGTTCTGTCCCCGAAAAACAAACCTCTACCAACACCA  
AGGCCCTATCCAAAACCTGCACCTTCAGCGGGAAAGACTACGTG**TGA**ACAGAGGCAAAAG  
GAGAAAATCATGTTGAAACAAACCGAAAATGGACATTGAGATACTATCATTAAACATTAGGAC  
CTTAGAATTGGGTATTGTAATCTGAAGTATGGTATTACAAAACAAACAAACAAAAAA  
ACCCATGTGTTAAACTCAGTCTAAACATGGCTTAACTTCTTATTTATCTTCTTCCTCA  
ATATAGGAGGGAAGATTTCATTGTATTACTGCTCCATTGAGTAATCATACTCAAAT  
GGGGGAAGGGGTGCTCTTAAATATATAGATATGTATATACATGTTTTCTATTAAAAA  
ATAGACAGTAAAATACTATTCTCATTATGTTGATACTAGCATACTTAAATATCTCTAAAAT  
AGGTAATGTATTAAATTCCATATTGATGAAGATGTTATTGGTATATTCTTCTTCGTCC  
TTATATACATATGTAACAGTCAAATATCATTACTCTCTTCAATTAGCTTGGGTGCCCTTG  
CCACAAGACCTAGCCTAATTACCAAGGATGAATTCTTCATTCTCATGCGTGCCCTTT  
CATATACTTATTTCATTACCATATCTTATAGCACTTGCATCGTTATTAGCCCTTAT  
TTGTTTGTGTTCTATTGGCTCTATCTCCTGAATCTAACACATTTCTAGCCTACATTAA  
GTTCTAAAGCCAAGAAGAATTATTACAAATCAGAACATTGGAGGCAAATCTTCATG  
ACCAAAGTGATAAATTCTGTTGACCTCCCACACAATCCCTGACTCTGACCCATAGCACT  
CTGTTTGTGTTGAAAATATTGTTCAATTGAGTAGCTGATGCTGATGCTGTTCCCCAGGGTGT  
AACACAACTTATTGATTGATTAAGCTACTTATTCTAGTTATATCCCCCTAAACT  
ACCTTTTGTCCCCATTCTTAATTGTATTGTTCCAAAGTGTAAATTATCATGCGTTTA  
TATCTCTTAATAAGGTGTGGTCTGTTGTCGAACAAAGTGTAGACTTCTGGAGTGATA  
ATCTGGTACAAATATTCTCTGTAGCTGTAAGCAAGTCACCTAATCTTCTACCTCTTT  
TTCTATCTGCCAAATTGAGATAATGATACTTAACCAGTTAGAAGAGGTAGTGTGAATATTAA  
TTAGTTATTAATTACTCTTATTCTTGAACATGAACATGCTATGTAGTGTCTTATTGCT  
CAGCTGGCTGAGACACTGAAGAAGTCACTGAACAAAACCTACACACATACCTTCT  
CACTGCCTTCCTCTCTACCAAGTCTATTCCACTGAACAAAACCTACACACATACCTTCT  
GTGGTTCAGTGCCTTCCTCTACCAAGTCTATTCCACTGAACAAAACCTACGCACATAC  
CTTCATGTGGCTCAGTGCCTTCCTCTACCAAGTCTATTCCATTCTCAGCTGTT  
GACATGTTGTGCTGTTCCATTAAACAACGTCTACTTTCCAGTCTGTACAGAAC  
CTATTCACCTGAGCAAGATGATGTAATGGAAAGGGTGTGGCACTGGTGTCTGGAGAAC  
GATTGAGTCTGGTGTATCAATCACCCTGTGTTGAGCAAGGCATTGGCTGCTGTA  
GCTTATTGCTTCACTGTAAGCGGTGGTTGTAATTCTGATCTCCCACACTGATG  
TTGTGGGATCCAGTGAGATAGAATACATGTAAGTGTGTTGTAATTAAAAAGTGCTAT  
ACTAAGGAAAGAATTGAGGAATTAACTGCATACGTTGGTGTCTTCAAATGTTGA  
AAATAAAAAAAATGTTAAG

## FIGURE 98

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52185
><subunit 1 of 1, 211 aa, 1 stop
><MW: 22744, pI: 8.51, NX(S/T): 1
MANAGLQLLGFIЛАFLGWIGAIVSTALPQWRIYSYAGDNIVTAQAMYEGLWMSCVSQSTGQI
QCKVFDSSLNLSSTLQATRALMVVGILLGVIAIFVATVGMKCMKCLEDEVQKMRMAVIGGA
IFLLLAGLAILVATAWYGNRIVQEFYDPMPTPVNARYEFGQALFTGWAASLCLGGALLCCSC
PRKTTSYPTPRYPKPAPSSGKDYV
```

**Important features:**

**Signal peptide:**

amino acids 1-21

**Transmembrane domains:**

amino acids 82-102, 118-142 and 161-187

**N-glycosylation site.**

amino acids 72-75

**PMP-22 / EMP / MP20 family proteins**

amino acids 70-111

**ABC-2 type transport system integral membrane protein**

amino acids 119-133

## FIGURE 99

TTCTGGCAAACCGGGCTNCAGCTGTTGGCCTCATCTGCCTCCTGGATGGATGGC  
GCCATCNTCACACTGCCCTCCCCAGTGGAGGATTTACTCCCTATGCTGGCGACAACATCG  
TGACCGCCCAGCCATGTACGAGGGCTGTGGATGTCCNGCGTGTGCAGAGCACCGGGCAG  
ATCCAGTGCAAAGTCCTTGACTCCTGCTGAATCTGAGCAGCACATTGCAAGCAACCGTGC  
CTTGATGGTGGTTGGCATCCTCCTGGGAGTGATAGCAATCTTGTGGCACCGTTGGCATGA  
AGTGTATGAAGTGCTTGGAAAGACGATGAGGTGCAGAAGATGAGGATGGCTGTCAATTGGGGC  
GCGATATTCCTTCTGCAGGTCTGGCTATTTAGTTGCCACAGCATGGTATGGCAATAGAAN  
CNTTCAACANTTCTATGACCCCTATGACCCAGTCATGCCAGGTACGAATTGGTCA  
GGCTCTCTTCACTGGCTGGCTGCTGCTCTGCCTCTGGGAGGTGCCCTACTTGCT  
GTTCCTGTCCC

## FIGURE 100

ACCCCTGACCCAACGCGGCCCGACCGNTTCATGGCCAAACGCAGGNCCTCCAGCTGTTGG  
GCTTCATTCTCCCCTCCTGGATGGACCAGGCGCCATCNTCAGCACTGCCCTGCCAGTG  
GAGGATTACTCCTATNCCGGCNACACATCGTGANCGCCAGGCCNTGTACGAGGGGCTGT  
GGATGTCCTGCGTGTGCGAGAGCACCGGGCAGATCCAGTGCAAAGTCTTGACTCCCTGCT  
GAATCTGAGCAGCACATTGCAAGCAACCGTGCCTGATGGTGGTTGGCATCCTCCTGGAG  
TGATAGCAATCTNNNTGCCACCGTTGTNNNTGAAGTGTATGAAGTGCTTGAAGACGATGA  
GGTGCAGAAGATGAGGATGGCTGTCATTGGGGCGCGATATTCTTGCAGGTCTGGCTA  
TTTAGTTGCCACAGCATGGTATGGCAATAGAACATCGTTCAAGAATTCTATGACCCTATGACCGA

## FIGURE 101

GGGCCGACCATTATCCAACCGGGNTCACTGTTGGCTCATCTCCCTCCTGGATGAANCAGCGC  
CATCNTCAGACTCCCTGCCCATGGAGATTTNNCCTATGCTGGCGACAACATCNTGACCCCC  
AGCCATGTACGAGGGGCTTGAACGTCNGCGTGTGCAGANCACCGGGCAGATCCAGTGCAA  
AGTCTTGACTCCTGCTGAATCTGNGCAGCACATTGCAGCAACCCNTGCCCTGATGGTGGT  
TGGCATTCCCTGGGAGTGATAGCAATCTTGCCACCGTTGGCATGAAGTGTATGAAGT  
GCTTGGAAAGACGATGAGGTGCAGAAGATGAGGATGGCTGTCATTGGGGCGCGATATTCCTT  
CTTGCAGGTCTGGCTATTNNNNGTTGCCACAGCATGGTATGGCAATAGAACGTTCAAGAAT  
TCTATGACCCCTATGACCCCAGTCAATGCCAGGTACGAATTGGTCAGGCTCTCTTCACTGGC  
TGGGCTGCTGCTCTCTGCCCTCTGGGAGGTGCCCTACTTGCTGTTCCCTGCGA

## FIGURE 102

ATTCTCCCTCCTGGATGGATCGCNCCACCGTCACATTGCCTTCCCCANTGGAGGATTNAC  
TCCTATGCTGGCGACAACATCGTGACCCCCCAGGCCATTACCGAGGGCTTGGATGTCNT  
GCNTGTCGCAGAGCACCGGGCAGATCCCAGTGCAAAGTCTTGACTCCTGCTGAATCTGAG  
CAGCACATTGCAAGCAACCCGTGCCTTGATGGGTTGGCATCCTCCTGGAGTGATAGCAAC  
CTTGTCGCCACCGTTGGCATGAAGTGTATGAAGTGCTTGGAAAGACGATGAGGTGCCAGAAG  
ATGAGGATGGCTGTCATTGGGGCGCGATATTCTTGCAGGTCTGGCTATTAGTNGC  
CACAGCATGGTATGGCAATAGANTNNTCNNNNNTCTATGACCCTATGACCCAGTCAATG  
CCAGGTACGAATTGGTCAGGCTCTTCACGGCTGGCTGCTGCTCTCTGCCTCTG  
GGAGGTGCCCTACTTGTGTTCCCTGTCCC

### **FIGURE 103**

AGAGCACCGGCAGATCCCAGTNCAAAGTCTTGACCCTGCTGAATCTGAGCAGCACATTNC  
AAGCAACCCCTTGCCTTGAAGGTGGTTGNCATCCCCCTGGAGTGAATAGCAATCTTGTG  
GCCACC GTTGGCATGAAGTNTATGAAGTGCTT GGAAGACGATGAGGTGCAGAAGATGAGGAT  
GGCTGT CATTGGGGCGCGAT ATTCTTGCAGGTCTGGCTATTTAGTNNCCACAGCAT  
GGTATGGCAATAGNATNNNTCGNGGNTTCTATGACCTATGACCCAGTCATGCCAGGTAC  
GAATTTGGTCAGGCTCTCTTCACTGGCTGGCTGCTGCTCTGCCTCTGGGAGGTGC  
CCTACTTTGCTGTT CCTGTCCCCGAA

## FIGURE 104

AGCAATGCCCTGCCCCAGTGGAGGATTAATTCTATGNTGGGACAACATTGTGACNGCCC  
AGGCCATGTACGGGGGGCTGTGGATGTCCTGCGTGTGCAGAGCACCGGGCAGATCCAGTGC  
AAAGTNTTGACTCCTGCTGAATTGAGCAGCACATTGCAAGCAACCCGTGCCTTGATGGT  
GGTTGGCATCTTCCTGGGAGTGATAGCAATCTTGTGCCACCGTGGNAATGAAGTGTATGA  
AGTGCTTCCAAGACGATGAGGTGCAGAAGATGAGGATGGCTGTCAATTGGGGCGCATAATT  
CTTNTTGCAAGGTCTGGCTATTAGTTGCCACAGCATGGTATGCCAATAGAATNGTTCAAGA  
ATTTTATGACCCTATGACCCAGTCAATGCCAGGTACGAATTGGTCAGGCTTNTTCAGTG  
GCTGGGCTGCTGCTNTTCTGCCTNTGGGAGGTGCCCTANTTGCTGTTCCCTGCGAACCC

## FIGURE 105

TCATAGGGGGCGCGATATTTTCTTGCAGGTNTGGTTATTTAGTTGCCACAGCATGGTA  
TGGCAATAGAATCGTTCAAGAATTNTATGACCCTATGACCCAGTCAATGCCAGGTACGAAT  
TTGGTCAGGCTCTNTCACTGGNTGGGCTGCTGCTCTNTNNGCCTNTGGGAGGTGCCCTA  
CTTGCTGTTCTG

## **FIGURE 106**

TTCCCTGGGATGGATCCGCCCATCNTCACATGCCCTGCCCNNTGGAGATTTACNCCTATGC  
TGGCGAACAAACATCNTGACCGCCCAGGCCATGTACGAGGGCTGTGAATGTCCTGCGTGTC  
CCAGAGCACCAGGGCAGATCCAGTGCAAAGTCTTGACTCCTGCTGAATCTGAGCAGCACAT  
TGCAAGCAACCNTGCCCTGATGGTGGTGGCATCCTCCTGGAGTGATAGCAATCTTGTGG  
CCACCGTTGGCATGAAAGTGTATGAAGTGCTTGGAAGACGATGAGGTGCAGAAGATGAGGAT  
GGCTGTCATTGGGGCGCGATATTCTTCTTGCAAGGTCTGGCTATTTAGNNGCACAGCAT  
GGTATGGCAATCAGACCCNNTCANAAACTCTATGACCTATGACCCAGTCAATGCCAGGTA  
CGAATTGGTCAGGCTCTCTCACTGGCTGGCTGCTCTCTGCCTTCTGGAGGTG  
CCCTACTTGCTGTTCCGTCCCCGAAAAACAACCTTTACCCACG

## **FIGURE 107**

CGGGGCTGCAGCTGTTGGGCTTCATCTCGCTTCTGGGATGGAATCGGCCCATCGTCAGCA  
CTGCCCTGCCCATGGAGGATTACTCNTATGCTGGCACAACATCGTACCCAGGCCA  
TGTACGAGGGGCTGTGGATGTCNGCGTGTGCAGAGCACCGGGCAGATCCAGTGCAAAGTCT  
TTGACTCCTTGCTGAATCTGAGCAGCACATTGCAAGCAACCNTGCCTTGATGGTGGTTGGCA  
TCCTCCTGGGAGTGATAGCAATCTTGCCACCGTTGGCATGAAGTGTATGAAGTGCTTG  
GAAGACGATGAGGTGCAGAAGATGAGGATGGCTGTCATTGGGGCGCGATATTCTTGC  
AGGTCTGGCTATTNTAGTTGCCACAGCATGGTATGGCAATAGAACGTTCAAGAATTCTAT  
GACCCTATGACCCCAGTCAATGCCAGGTACGAATTGGTCAGGCTCTCTCACTGGCTGGC  
TGCTGCTTCTCTGCCTCTGGGAGGTGCCCTACTTGTGTTGCAGAA

## FIGURE 108

GCCTGCCGTCACTGCCGGCACCGCGGCCCTGCCCTGCCCTCCGCCCTGCCCTGCAC  
CGCGTAGACCGACCCCCCCCCTCCAGCGGCCACCCGGTAGAGGACCCCCGCCGTGCCCG  
ACCGTCCCCGCCCTTTGTAAAACCTAAAGCAGGGCGCAGCATTACGTTCCGCCCGGT  
GACCTCTCAGGGTCTCCCCGCCAAGGTGCTCCGCCGCTAACCGAACATGGCGAAGGTGGAG  
CAGGTCTGAGCCTCGAGCCGAGCACGCTCAAATTCCGAGGTCCCTCACCGATGTTGT  
CACCAACCTAAAGCTTGGCAACCCGACAGACGAAATGTGTGTTAACGGTAAGACTA  
CAGCACCAACGTTAGGTACTGTGTGAGGCCAACAGCGGAATCATCGATGCAGGGCCTCAATT  
AATGTATCTGTGATGTTACAGCCTTCGATTATGATCCAATGAGAAAAGTAAACACAAGTT  
TATGGTCAGTCTATGTTGCTCCAATGACACTTCAGATATGGAAGCAGTATGGAAGGAGG  
CAAACCGGAAGACCTTATGGATTAAAACCTAGATGTGTTGAATTGCCAGCAGAGAAT  
GATAAACCACATGATGTAGAAATAAAATTATCCACAATGCATCAAAGACAGAAC  
ACCAATAGTGTCTAAGTCTGAGTTCTTGGATGACACCGAACGTTAAGAAGGTTATGG  
AAGAATGTAAGAGGCTGCAAGGTGAAGTTAGAGGCTACGGGAGGAGAACAGCAGTTCAAG  
GAAGAAGATGGACTGCGGATGAGGAAGACAGTGCAGAGCAACAGCCCCATTTCAGCATTAGC  
CCCAACTGGGAAGGAAGAACAGCCTTAGCACCCGGCTTGGCTCTGGTGGTTTGTCTTTA  
TCGTTGGTGTATTATTGGGAAGATTGCTTGAGAGGTAGCATGCACAGGATGGTAAATTG  
GATTGGTGGATCCACCATATCATGGGATTAAATTATCATAACCAGTGTAAAAGAAATT  
AATGTATGATGACATCTCACAGGTCTGCCTTAAATTACCCCTCCCTGCACACACATACAC  
AGATAACACACACAAAATATAATGTAACGATCTTTAGAAAGTTAAAATGTATAGTAACG  
ATTGAGGGGGAAAAAGAATGATCTTATTAAATGACAAGGGAAACATGAGTAATGCCACAAT  
GGCATATTGTAAATGTCATTAAACATTGGTAGGCCTGGTACATGATGCTGGATTACCTC  
TCTTAAATGACACCCCTCCTCGCCTGGTGGCTGGCCCTGGGAGCTGGAGGCCAGCAT  
GCTGGGAGTGCAGCTCCACACAGTAGTCCCCACGTGGCCACTCCGGCCAGGCTG  
CTTCCGTGTCTCAGTTCTGTCCAAGCCATCAGCTCCGGACTGATGAACAGAGTCAGA  
ACCCCAAAGGAATTGCACTGGCAGCATCAGACGTACTCGTCATAAGTGAGAGGCGTGTG  
TGACTGATTGACCCAGCGCTTGGAAATAATGGCAGTGCTTGTCACTTAAAGGGACAA  
GCTAAATTGTATTGGTCATGTAGTGAAGTCAAACGTATTAGAGATGTTAATGCATA  
TTAACCTATTAAATGTATTCTCATCTCATGTTCTTATTGTACAAGAGTACAGTTAATGC  
TCGCTGCTGCTGAACCTCTGTTGGTGAACGGTATTGCTGCTGGAGGGCTGTGGCTCCT  
GTCTCTGGAGAGTCTGGTATGGAGGTGGGTTATTGGGATGCTGGAGAAGAGCTGCCA  
GGAAGTGTGTTCTGGTCAGTAAATAACAACTGTCAAGGGAGGGAAATTCTCAGTAGTG  
ACAGTCACACTAGGTTACCTTTAAATGAAGAGTAGTCAGTCTCTAGATTGTTCTTATA  
CCACCTCTCAACCATTACTCACACTTCCAGCGCCCAGGTCCAAGTCTGAGCCTGACCTCCCC  
TTGGGGACCTAGCCTGGAGTCAGGACAAATGGATGGCTGCAGAGGGTTAGAAGCGAGGGC  
ACCAGCAGTTGTGGTGGGAGCAAGGGAAAGAGAGAAACTCTTCAGCGAATCCTCTAGTAC  
TAGTTGAGAGTTGACTGTGAATTAAATTATGCCATAAAAGACCAACCCAGTTCTGTTGA  
CTATGTAGCATCTGAAAAGAAAAATTATAATAAAAGCCCCAAAATTAAGAAAA

## **FIGURE 109**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53977
<subunit 1 of 1, 243 aa, 1 stop
<MW: 27228, pI: 7.43, NX(S/T): 2
MAKVEQVLSLEPQHELKFRGPFTDVVTNLKLGNPTDRNVCFKVTTAPRRYCVRPNSGIID
AGASINVSVMLQPFDYDPNEKSCHKFMVQSMFAPTDTSDMEAVWKEAKPEDLMDSKLRCVFE
LPAENDKPHDVEINKIISTTAKTETPIVSKSLSSSLDDTEVKVMEECKRLQGEVQLREE
NKQFKEEDGLRMRKTVQSNSPISALAPTGKEEGLSTRLLALVVLFFIVGVIIGKIAL
```

**Important features:**

**Transmembrane domain:**

amino acids 224-239

**N-glycosylation site.**

amino acids 68-71

**N-myristoylation site.**

amino acids 59-64, 64-69 and 235-240

## **FIGURE 110**

GTCAGTCTTAGATTGCTTATCCCACCTTCAACCANTACTCACATTCNAGCGCCAG  
GTCCANGTCTGAGCCTGACTCCCCCTGGGGACCTAGCCTGGAGTCAGGACAATGGNTCGGG  
CTGCAGAGGNTTAGAAGCGAGGGCACCAGCAGTTGGGTGGGAGCAAGGGNNAGAGAAA  
CTCTTCAGCGAACCTCTAGTACTAGTTGAGAGTTGACTGTGAATTAAATTATGCCATA  
AAAGACNAACCCAGTTCTGTTGACTATGTAGCATCTGAAAAGAAAAATTATAATAAAGCC  
CCAAAATTAAGAATTCTTTGTCATTTGTCACATTGCTCTATGGGGGAATTATTATTTT  
ATCATTTTTATTATTTGCCATTGGAAGGTTAACTTTAAAATGAGC

## **FIGURE 111**

TATTGTAAAGGCCATTTAAACCATTGGTAGGCCTGGTACATGATGCTGGATTACCTCCTT  
AAATGACACCNTTCCTCGCCTGTTGGTGCCTGGCCNTTGGGGAGCTGGAGCCCCAGCATGCTG  
GGGAGTGCCTCAGCTCCACACAGTAGTCCCCACGTGGCCACTCCGGCCCAGGCTGCTTT  
CCGTGTCTTCAGTTCTGTCCAAGCCATCAGCTCCTGGACTGATGAACAGAGTCAGAACGCC  
CAAAGGAATTGCCACTGTGGCAGCATCAGACGTACTCGTCATAAGTGAGAGGCGTGTGTTGA  
CTGATTGACCCAGCGCTTGGAAATAATGGCAGTGCTTGTTCACTTAAAGGGACCAAGCT  
AAATTGTATTGGTCATGTAGTGAAGTCAAACTGTTATTCAAGAGATGTTAATGCATATTTA  
ACTTATTTAATGTATTCATCTCATGTTTCTTATTGTCACAAGAGTACAGTTAATGCTGCG  
TGCTGCTGAACCTGTTGGGTGAACGGTATTGCTGGAGGGCTG

## **FIGURE 112**

CCCTGGTGGTTTGTCTTAATTCGTTGGTGTATTNTGGAAAGATTGCTTAGAGGTA  
GNATGCACCNGGCTGGTAAATTGGATTGGTGGATCCACCATATCCATGGGATTAAATTAT  
CATAACCATGTGTAAAAAGAAATTAATGTATGACATNTCACAGGTATTGCCTTAAATT  
ACCCATCCCTGNANACACATACACAGATAACACANANACAAATNTAATGTAACGATNTTTAG  
AAAGTTAAAAATGTATAGTAAC

## **FIGURE 113**

GGTGGCCCATTCCCGGCCAGGCTGCTTCGGTNTTCAGTTCTGTCCAAGCCATCAGCTCC  
TTGGGACTGATGAACAGAGTCAGAAGCCAAAGGAATTGCACTGTGGCAGCATNAGACGTAC  
TTGTNATAAGTGAGAGGCCTGTTGACTGATTGACCCAGCGCTTGGAAATAATGGCAGT  
GCTTTGTTCANTTAAAGGGACCAAGCTAAATTGTATTGGTCATGTAGTGAAGTCAAACTG  
TTATTCAAGAGATGTTAACATGCATATTTAANTTATTTAATGTATTTNATNTCATGTTTCTTA  
TTGTCACAAGAGTACAGTTAACATGCTGCGTGCTGAANTNTGTTGGGTGAACGGTATTGC  
TGCTGGAGGGCTGTGGGCTCCTCTGTCTTGGAGAGTCTGGTCATGTGGAGGTGGG

## FIGURE 114

TGCTTCCGTCTCAGTTCTGTCCAAGCCATCAGCTCCTGGGACTTGATGAACAGAGTC  
AGAAGCCCAAAGGAATTGCACGTGGCAGCATCAGACGTACTCGTCATAAGTGAGAGGGGTG  
TGTTGACTGATTGACCCAGCGCTTGGAAATAATGGCAGTGCTTGTTCACTTAAAGGGAC  
CAAGCTAAATTGTATTGGTTCATGTAGTGAAGTCAAACTGTTATTAGAGATGTTAACAGTAA  
ATATTTAACTTATTAATGTATTCATCTCATGTTCTTATTGTCACAAGAGTACAGTTAA  
TGCTGCGTGC

## **FIGURE 115**

AAACCTTAAAAGTTGAGGGAAAAGAATGATCCTTATTAATGACAAGGGAAACNTGN  
AATGCCACAATGGCATATTGTAAATGTCATTTAACATTGGTAGGCCTGGTACATGATGC  
TGGATTACCTCTCTTAAATGACACCCTCCTCGCCTGGTCTGGCCCTGGGAGCTN  
GAGCCCAGCATGCTGGGAGTGCGGTCTGCTCACACAGTAGTCCCCANGTGGCCANTCCC  
GGCCCAGGCTGCTTCCGTCTTCAGTTCTGCCAAGCCATCAGCTCCTGGANTGATGA  
ACAGAGTCAGAACCCAAAGGAATTGCANTGTGGCAGCATCAGANTANTNGTCATAAGTGA  
GAGGCGTGTGTTGANTGATTGACCCAGCGCTTGGAAATAATGGCAGTGCTTGTTCAN  
AAAGGGNCCAAGNTAAATTGTATTGGTCATGTAGTGAAGTCAAANTGTTATTCAAGAGATG  
TTAATGCATATTAANTTATTAATGTATTCATNTCATGTTCTTATTGTCACAAGGGT  
ACAGTTAATGCTGCGTGTGAANTCTGTTGGGTGAANTGGTATTGCTG

## **FIGURE 116**

GGCCCTTGGGAGCTGGAGCCCAGCATGCTGGGAGTCAGCTCCACACAGTAGTCCC  
CACGTGGCCCCTCCGGCCAGGCTGCTTCGTCTCAGTTCTGTCCAAGCCATCAGC  
TCCTTGGACTGATGAACAGAGTCAGAACGCCAAAGGAATTGCAGTGCGCATCAGACG  
TACTCGTCATAAGTGAGAGGGGTGTGTTGACTGATTGACCCAGCGCTTGAAATAATGGC  
AGTGCTTGTTCACTTAAAGGGACCAAGCTAAATTGTATTGGTCATGTAGTGAAGTCAAA  
CTGTTATTCAAGAGATGTTAATGCATATTAACCTATTAAATGTATTCATCTCATGTTTC  
TTATTGTACAAGAGTACAGTTAATGCTGCGTGTGACTCTGTTGGGTGAACGGTAT  
TGCTGCTGGAGGGCTGTGGCTCCTCTGTCTGGAGAGTCTGGTCATGTGGAGGTGGG

## **FIGURE 117**

GCGAGCTCGGGTGCCTGGCCCGGCCCTGGCGGGCGGCCTCCGGCTCAGGCTGGCTGAGA  
GGCTCCCAGCTGCAGCGTCCCCGCCCTCCTCGGGAGCTCTGATCTCAGCTGACAGTGCC  
CTCGGGGACCAAACAAGCCTGGCAGGGTCTCACTTTGTTGCCAGGCTGGAGTTAGTGCA  
TGATCATGTTACTGCAGCCTGACCTCCTGGGTTCAAGCGATCCTGCTGAGTAGCTGGGA  
CTACAGGACAAAATTAGAAGATCAAATGGAAAATATGCTGCTTGGTTGATATTTTCACC  
CCTGGGTGACCTCATTGATGGATCTGAAATGGAATGGGATTTATGTCAGGACTTGAGAAA  
GGTACCCGGATTGTCACTGAAAGGACTTCCATCTCACAGCCCCGATTGAGGCAGATG  
CTAAGATGATGGTAAATAACAGTGTGGCATCGAACATGCCAGAAAGAAACTCCAACCTCCAGC  
CTTCTGAATTGGAGGATTATCTTCTATGAGACTGTCTTGAGAACATGGCACCCGAAACCTT  
AACCAAGGGTGAAAGTTCAAGATTGGTTCTTGAGCCACTAAAATATCACCAACAAAGGGAG  
TATCTGTTAGGAGAAAGAGACAGGTGTATGGCACCGACAGCAGGTTAGCATCTGGACAAA  
AGGTTCTAACCAATTCCCTTCAGCACAGCTGTGAAGCTTCCACGGGCTGAGTGGCAT  
TCTCATTCCCTCAGCATGTTCTAACTGCTGCCACTGTGTTAGTGGAAAGGACTATG  
TCAAAGGGAGTAAAAGCTAAGGGTAGGGTTGTAAGATGAGGAATAAAAGTGGAGGCAAG  
AACGTCGAGGTTCTAAGAGGGAGCAGGAGAGAACAGTAGTGGTGGTACCAAAAGAGAGGGTAC  
CAGAGAGCATCTGCAGGAGAGAGCGAAGGGTGGAGAAGAAGAAAAAAATCTGGCCGGGGTC  
AGAGGATTGCCAAGGGAGGCCTCCCTTCAGTGGACCCGGGTCAGAACATCCACATTCCG  
AAGGGCTGGCACGAGGAGGCATGGGGACGCTACCTGGACTATGACTATGCTCTCTGGA  
GCTGAAGCGTGCTCACAAAAGAAATACATGGAACCTTGGAAATCAGCCCAAGATCAAGAAA  
TGCCTGGTGAATGATCCACTCTCAGGATTGATAACGATAGGGCTGATCAGTTGGTCTAT  
CGGTTTGCACTGTCGACGAATCCAATGATCTCCTTACCAAAACTGCGATGCTGAGTC  
GGGCTCCACCAGGTTGGGGCTATCTGCGTCTGAAAGATCCAGACAAAAAGAATTGGAAGC  
GCAAAATCATTGCGGTCTACTCAGGGCACCAGTGGGTGGATGTCCACGGGTTCAAGAAGGAC  
TACAACGTTGCTGTCGATCACTCCCTAAAATACGCCAGATTGCTCTGGATTACCG  
GAACGATGCCAATTGTGCTTACGGTAACAGAGACCTGAAACAGGGCGGTATCATCTAAA  
TCACAGAGAAAACCAGCTCTGCTTACCGTAGTGAGATCACTTCATAGGTTATGCCTGGACTT  
GAACCTGTCAATAGCATTCAACATTTCAAAATCAGGAGATTTCGTCCATTAAAAAA  
TGTATAGGTGCAGATATTGAAACTAGGTGGGACTTCAATGCCAAGTATATACTCTTCTTIA  
CATGGTGTGAGTTTCAATTGTTAGAAAAATTGTTGCTTCTTAAAGAATAGACACACTTT  
AAACCTTCAAACAGGTATTATAAAACATGTGACTCCTTAATGGACTTATTCTCAGGGTCC  
TACTCTAAGAAGAATCTAATAGGATGCTGGTTGTATTAAATGTGAAATTGCATAGATAAA  
GGTAGATGGTAAAGCAATTAGTATCAGAAATAGAGACAGAAAGTTACAACACAGTTGACTA  
CTCTGAGATGGATCCATTAGCTCATGCCCTCAATGTTATATTGTTATCTGTTGGGTCT  
GGGACATTAGTTAGTTTGAAGAATTCAAATCAGAAGAAAAGCAAGCATTATAAA  
CAAAACTAATAACTGTTTACTGCTTAAGAAAATAACAAATTACAATGTGTTATTATTTAAAAA  
TGGGAGAAATAGTTGTTCTATGAAATAAACCTAGTTAGAAATAGGGAAGCTGAGACATT  
TAAGATCTCAAGTTTATTAACTAATCTCAAATATGGACTTTCATGTATGCATAGGG  
AAGACACTCACAAATTATGAATGATCATGTGTTGAAAGCCACATTATTTATGCTACAT  
TCTATGTATGAGGTGCTACATTAGGACAAAGAATTCTGTAATCTTTCAAGAAAGAGT  
CTTTTCTCCTTGACAAATCCAGTTGTATGAGGACTATAGGGTGAATTCTCTGATTAG  
TAATTAGATATGTCCTTCTTAAAGAATAAAATTATGAATATGA

## **FIGURE 118**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57253
<subunit 1 of 1, 413 aa, 1 stop
<MW: 47070, pI: 9.92, NX(S/T): 3
MENMLLWLIFFTPGWTLIDGSEMEWDFMWHLRKVPRIVSERTFHLTSPAFAEADAKMMVNTVC
GIECQKELPTPSLSELEDYLSYETVFENGTRTLTRVKVQDLVLEPTQNITTKGVSVRRKRQV
YGTDSRFSILDKRLFNTFPFSTAVKLSTGCSGILISPQHVLAAHCVHDGKDVKGSKKLRV
GLLKMRNKGKRRGSKRSRREASGGDQREGTREHLQERAKGGRRKKSGRGQRIAEGRPS
FQWTRVKNTHIPKGWARGGMGDATLDYDYALLELKRAHKKKYMELGISPTIKKMPGGMIHFS
GFDNDRADQLVYRFCSVSDESNDLLYQYCDAESGSTGSGVYRLKDSDKKNWKRKIIAVYSG
HQWVDVHGVQKDYNNAVIRTPLKYAQICLWIHGNDANCAYG
```

**Important features:**

**Signal peptide:**

amino acids 1-16

**N-glycosylation sites.**

amino acids 90-93, 110-113 and 193-196

**Glycosaminoglycan attachment site.**

amino acids 236-239

**Serine proteases, trypsin family, histidine active site.**

amino acids 165-170

## FIGURE 119

AATGTGAGAGGGCTGATGGAAGCTGATAGGCAGGACTGGAGTGTAGCACCACTGGAT  
GTGACAGCAGGCAGAGGAGCACTTAGCAGCTTATTCACTGTCCGATTCTGATTCCGGCAAGG  
ATCCAAGCATGGAATGCTGCCCGTCGGCAACTCCTGGCACACTGCTCCTCTTCTGGCTTC  
CTGCTCCTGAGTTCCAGGACCACGCTCCGAGGAGGACCGGGACGGCTATGGGATGCCTG  
GGGCCCATGGAGTGAATGCTCACGCACCTGCAGGGGGAGGGGCTCCTACTCTTGAGGCGCT  
GCCTGAGCAGCAAGAGCTGTGAAGGAAGAAATATCCGATACAGAACATGCAGTAATGTGGAC  
TGCCCCACCAGAAGCAGGTGATTCCGAGCTCAGCAATGCTCAGCTCATAATGATGTCAAGCA  
CCATGCCAGTTTATGAATGGCTCCTGTCTAATGACCTGACAACCCATGTTCACTCA  
AGTGCCAAGCAAAGGAACAACCTGGTTGTTGAACACTGACACCTAAGGTCTTAGATGGTACG  
CGTTGCTATACAGAACTTGGATATGTGCATCAGTGGTTATGCCAAATTGTTGGCTGCGA  
TCACCACTGGGAAGCACCGTCAAGGAAGATAACTGTGGGGCTGCAACGGAGATGGTCCA  
CCTGCCGGCTGGTCCGAGGGCAGTATAAATCCCAGCTCTCCGCAACCAAATGGATGATACT  
GTGGTTGCACCCATGGAAGTAGACATATTGCCTTGTCTAAAAGGTCTGATCACTT  
ATATCTGGAAACCAAAACCTCCAGGGACTAAAGGTAAAACAGTCTCAGCTCACAGGAA  
CTTCCTTGTGGACAATTCTAGTGTGGACTTCCAGAAATTCCAGACAAAGAGATACTGAGA  
ATGGCTGGACCACTCACAGCAGATTTCATTGTCAAGATTGTAACCTGGGCTCCGCTGACAG  
TACAGTCCAGTCATCTTCTATCAACCCATCATCCACCGATGGAGGGAGACGGATTCTTTC  
CTTGCTCAGCAACCTGTGGAGGGTTATCAGCTGACATCGGCTGAGTGCACGATCTGAGG  
AGCAACCGTGTGGTGTGACCAACTGTCACTATTACCCAGAGAACATCAAACCAAACC  
CAAGCTTCAGGAGTGCAACTTGGATCCTGTCCAGCCAGTGACGGATAACAGCAGATCATGC  
CTTATGACCTCTACCATCCCCCTCCTCGGTGGAGGCCACCCATGGACCGCGTGCCTCC  
TCGTGTGGGGGGGCATCCAGAGCCGGCAGTTCTGTGGAGGGAGGACATCCAGGGCA  
TGTCACTTCAGTGGAAAGAGTGGAAATGCATGTACACCCCTAACAGATGCCATCGCGAGCCCT  
GCAACATTTTGACTGCCCTAAATGGCTGGCACAGGAGTGGTCTCCGTGCACAGTGACATGT  
GCCAGGGCCTCAGATACCGTGTGGCCTCTGCATCGACCATCGAGGAATGCACACAGGAGG  
CTGTAGCCCCAAAACAAAGCCCCACATAAAAGAGGAATGCATCGTACCCACTCCCTGCTATA  
AACCCAAAGAGAAACTCCAGTCAGGGCCAAGTTGCCATGGTCAAACAGCTCAAGAGCTA  
GAAGAAGGAGCTGCTGTCAAGAGGAGCCCTCGTAAGTTGAAAGCACAGACTGTTCTATA  
TTTGAAGACTGTTTGTAAAGAAAGCAGTGTCTCACTGGTTGAGCTTCATGGGTTCTGA  
ACTAAAGTGTAAATCATCTCACCAAGCTTTGGCTCTCAAATTAAAGATTGATTAGTTCAA  
AAAAAA

## FIGURE 120

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58847
<subunit 1 of 1, 525 aa, 1 stop
<MW: 58416, pI: 6.62, NX(S/T): 1
MECCRATPGTLLLFLAFLSSRTARSEEDRGLWDAGPWSECSRTCGGASYSLRRCLS
SKSCEGRNIRYRTCSNVDCPPEAGDFRAQQCSAHNDVKHHGQFYEWLPVSNDPDNPCSLKCQ
AKGTTLVVELAPKVLGTRCYTESLDMCISGLCQIVGCDHQLGSTVKEDNCGVNGDGSTCR
LVRGQYKSQLSATKSDDTVVALPYGSRHIRLVLKGPDHLYLETKTLQGTKGENSLSTGTFL
VDNSSVDFQKFPDKEILRMAGPLTADFIVKIRNSGSADSTVQFIFYQPIIHRWRETDFFPCS
ATCGGGYQLTSAECYDLRSNRVVADQYCHYYPPENIKPKPKLQECNLDPASPASDGYKQIMPYD
LYHPLPRWEATPWTACSSSCGGGIQSRAVSCVEEDIQGHVTSVEEWKCMYTPKMPIAQPCNI
FDCPKWLAQEWSPTVTCGQGLRYRVVLCIDHRGMHTGGCSPKTYPHIKEECIVPTPCYKPK
EKLPVEAKLPWFKQAQELEEGAAVSEEPS
```

**Important features:**

**Signal peptide:**

amino acids 1-25

**N-glycosylation site.**

amino acids 251-254

**Thrombospondin 1**

amino acids 385-399

**von Willebrand factor type C domain proteins**

amino acids 385-399, 445-459 and 42-56

## FIGURE 121

CGGACGCGTGGCGCGCTCGGAACCTCCGTGGAGGGCCGGTGGGCCCTCGGCCTGAC  
AGATGGCAGTGGCCACTGCGGCAGTACTGGCGCTCTGGCGGGCGCTGTGGCTGGCG  
GCCCGCCGGTTCGTGGGCCAGGGTCCAGCGCTGCGCAGAGGCGGGACCCGGCCTCAT  
GCACGGGAAGACTGTGCTGATCACCGGGCGAACAGCGGCCTGGCCGCCACGCCGCCG  
AGCTACTGCGCCTGGGAGCGCGGGTGATCATGGCTGCCGGACCGCGCGGCCAGGGAG  
GCGGCGGGTCAGCTCCGCCGAGCTCCGCCAGGCCGGAGTGCAGCCTGGCGT  
CAGCGGGGTGGCGAGCTCATAGTCGGAGCTGGACCTCGCCTCGCTGCCTCGGTGCGC  
CCTTCTGCCAGGAAATGCTCAGGAAGAGCCTAGGCTGGATGTCTGATCAATAACGCAGGG  
ATCTTCCAGTGCCCTTACATGAAGACTGAAGATGGTTGAGATGCAGTCGGAGTGAACCA  
TCTGGGCACTTCTACTCACCAATCTTCTCCTGGACTCCTCAAAAGTCAGCTCCCAGCA  
GGATTGTGGTAGTTCTTCAAACTTATAAATACGGAGACATCAATTGATGACTTGAAC  
AGTGAACAAAGCTATAATAAAAGCTTTGTTAGCCGGAGCAAACGGCTAACATTCTTT  
TACCAGGGAACTAGCCCGCCGCTTAGAAGGCACAAATGTCACCGTCAATGTGTTGCATCCTG  
GTATTGTACGGACAAATCTGGGAGGCACATACACATTCCACTGTTGGTCAAACCACTCTTC  
AATTGGTGTACGGCTGCTAAAGTAGGAACAAGGAGTAAAAGAGCTGTTATAAAACTGCATATCAG  
TTATATCTGTGATCAGGAATGGTGTGGATTGAGAACTTGTACTTGAAGAAAAAGAATTG  
ATATTGGAATAGCCTGCTAACAGGATACATGTGGTATTGGAGTTACTGAAAAATTATTT  
TGGGATAAGAGAATTCAAGCAAAGATGTTAAATATATAGTAAGTATAATGAATAATAA  
GTACAATGAAAAATACAATTATATTGAAACATTATAACTGGCAAGCATGGATGACATATTA  
ATATTGTCAGAATTAAAGTGAACCAAAGTGCATCGAGAGGTTTCAAGTATCTTGAGTT  
TCATGCCAAAGTGTAACTAGTTACTACAATGTTGGTGTGGAAATTATCTGC  
CTGGTGTGCACACAAGTCTTACTTGAATAAATTACTGGTAC

## FIGURE 122

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58747
<subunit 1 of 1, 336 aa, 1 stop
<MW: 36865, pI: 9.15, NX(S/T) : 2
MAVATAAAVLAALGGALWLAARRFVGPRVQRLRRGGDPGLMHGKTVLITGANSGLGRATAAE
LLRLGARVIMGCRDRARAEEAAGQLRRELRQAAECGPEPGVSGVGELIVRELDLASLRVRA
FCQEMLQEEPRLDVLINNAGIFQCPYMKTEDGFEMQFGVNHLGHFLLTNLLLGLLKSSAPSR
IVVVSSKLYKYGDINFDDLNEQSYNKSFCYSRSKLANILFTRELARRLEGTVNVNLHPG
IVRTNLGRHIHIPLLVKPLFNLVSWAFFKTPVEGAQTSIYLASSPEVEGVSGRYFGDCKEEE
LLPKAMDESVARKLWDISEVMVGLLK
```

**Important features:**

**Signal peptide:**

amino acids 1-21

**Short-chain alcohol dehydrogenase family protein**

amino acids 134-144, 44-56 and 239-248

**N-glycosylation site.**

amino acids 212-215 and 239-242

## FIGURE 123

GGGGATTGTAAAGAGGAAGNACTGTGCCAAAGNTATGGATGAATCTGTTGCAAGAAAATTN  
TGGGATATCAGTGAAGTGTGGTTNGCCTGCTAAAATAGGAACAAGGAGTAAAAGAGCTGTT  
TATAAAACTGCATATCAGTTATATCTGTGATCAGGAATGGTGTGGATTGAGAACTTGTACT  
TGAAGAAAAAGAATTGATATTGGAATAGCCTGNTAACAGGNAACATGTGGTATTGGAG  
TTACTGAAAAATTATTTGGATAAGAGAATTTCAGCAAAGATGTTAAATATATAGT  
AAGTATAATGAATAATAAGTACAATGAAAATACAATTATATTGTAAAATTATAACTGGCA  
AGCATGGATGACATATTAATATTGTCAGAATTAAAGTGACTCAAAGTGCTATCGAGAGGTTT  
TTCAAGTATCTTGAGTTCATGGCAAAGTGTAACTAGTTTACTACAATGTTGGTGT  
TGTGTGGAAATTATCTGCCTGGCTT

## FIGURE 124

GAGAGGACGAGGTGCCGCTGCCCTGGAGAATCCTCCGCTGCCGTGGCTCCGGAGCCCAGCC  
CTTCCTAACCAACCAACCTAGCCCAGTCCAGCCGCCAGCGCCTGTCCCTGTACGGAC  
CCCAGCGTTACCATGCATCCTGCCGTCTTCTATCCTTACCCGACCTCAGATGCTCCCTCT  
GCTCCTGGTAACTGGGTTTTACTCCTGTAACAACGTAAAGTCTGCTACAGAGA  
ATATAGATGAAATTAAACAATGCTGATGTTGCTTAGTAAATTATGCTGACTGGTGT  
CGTTTCAGTCAGATGTTGCATCCAATTGGAGGAAGCTCCGATGTCATTAAGGAAGAATT  
TCCAAATGAAAATCAAGTAGTGTGCTCCAGAGTTGATTGTGATCAGCACTCTGACATAGCCC  
AGAGATAACAGGATAAGCAAATACCAACCCCTCAAATTGTTGTAATGGATGATGAAG  
AGAGAATAACAGGGTCAGCGATCAGTGAAAGCATTGGCAGATTACATCAGGCAACAAAAAG  
TGACCCCCATTCAAGAAATTGGGACTTAGCAGAAATCACCCTTGTGATCGCAGCAAAAGAA  
ATATCATTGGATATTGGAGCAAAGGACTCGGACAACATAGAGTTGAAACGAGTAGCG  
AATATTTGCATGACTGTGCCCTTCTTCATGGGATGTTCAAAACCGGAAAG  
ATATAGTGGCGACAACATAATCTACAAACCACCAGGGCATTCTGCTCCGGATATGGTGTACT  
TGGGAGCTATGACAATTGATGTGACTTACAATTGGATTCAAGATAATGTGTTCTCTT  
GTCCGAGAAATAACATTGAAAATGGAGAGGAATTGACAGAAGAAGGACTGCCTTCTCAT  
ACTCTTCACATGAAAGAAGATAACAGAAAGTTAGAAATATTCCAGAATGAAGTAGCTCGGC  
AATTAATAAGTAAAAAGGTACAATAACCTTTACATGCCATTGTGACAAATTAGACAT  
CCTCTTCTGCACATACAGAAAACCTCCAGCAGATTGTCTGTAATCGCTATTGACAGCTTAG  
GCATATGTATGTGTTGGAGACTTCAAAGATGTATTAATTCTGGAAAACCTCAAGCAATTG  
TATTTGACTTACATTCTGGAAAACCTGCACAGAGAATTCCATCATGGACCTGACCCAACGTGAT  
ACAGCCCCAGGAGAGCAAGCCAAGATGTAGCAAGCAGTCCACCTGAGAGCTCCTCCAGAA  
ACTAGCACCCAGTGAATATAGGTATACTCTATTGAGGGATCGAGATGAGCTTAAAAACTTG  
AAAAACAGTTGTAAGCCTTCAACAGCAGCATCACCTACGTGGTGGAAATAGTAAACCTA  
TATTTCTATAATTCTATGTGTTATTTGAAATAACAGAAAGAAATTAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## FIGURE 125

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57689
<subunit 1 of 1, 406 aa, 1 stop
<MW: 46927, pI: 5.21, NX(S/T): 0
MHPAVFLSLPDLRCSLLLVTWVFTPVTTEITSLATENIDEILNNADVALVNFYADWCRFSQ
MLHPIFEASDVIKEFPNENQVFARVDCDQHSDIAQRYRISKYPTLKLFRNGMMMKREYR
GQRSVKALADYIRQQKSDPIQEIRDLAETTLDRSKRNIIGYFEQKDSNDNYRVFERVANILH
DDCAFSAFGDVS KPERYSGDNIIYKPPGHSAPDMVYLGAMTNFDVTYNWIQDKCVPLVREI
TFENGEELEEGLPFLILFHMKEDTESLEIFQNEVARQLISEKGTINFLHADCDKFRHPLLH
IQKTPADCPVIAIDSFRHMYVFGDFKDVLIPGKLQFVFDLHSGKLHREFHHGPDTDTAPG
EQAQDVASSPPESSFQKLAPSEYRYTLLRDRDEL
```

**Important features:**

**Signal peptide:**

amino acids 1-29

**Endoplasmic reticulum targeting sequence.**

amino acids 403-406

**Tyrosine kinase phosphorylation site.**

amino acids 203-211

**Thioredoxin family proteins**

amino acids 50-66

## **FIGURE 126**

ATTAAGGAAGAATTCCAAATGAAAATCAAGTAGTNTTGCCAGAGTNGATTGTGATCAGCA  
CTCTGACATAGCCCAGAGATAAGCAAATACCCAACCCTCAAATTGTTCGTAATG  
GGATGATGATGAAGAGAGAACAGGGGTCAAGCGATCAGTGAAAGCATTGGCAGATTA

## **FIGURE 127**

AGAGGCCTCTGGAAAGTTGTCGGGGTGGTCCGCGCNGGAGGCCGGGTGAGAGGACNAGG  
TGCCGCTGCCTGGAGAACATCCTCCGCTGCCGTGGCTCCGGAGCCCAGCCCTTCTTAACCC  
AACCCAACCTAGCCNGTCCCAGCCGCCAGCGCCTGTCCTGTCNCGGANCCCAGCGTNACC  
ATGCATCCTGCCGTCTCCTATCCTTACCCGACCTCAGATGCTCCCTCTGCTCCTGGTAAC  
TTGGGTTTTACTCCTGTAACAACGTAAATAACNNGTCTGATAACNNAGAATATAGATGAAA  
TTTTAAACNATGCTGATGTGGCTTAGTCATTTTATGCTGACTGGTGTCTTCAGTCAG  
ATGTGGCATCCAATTGGAGGANGCTTCCGATGTCATTAAGGAAGAATTCCAAATGAAAA  
TCAAGTAGTGTGTTGCCAGAGTTGATTGTGATCAGCACTCTGACATAGCCCAGAGATAAGGA  
TAAGCAAATACCCAAACCTCAAATTGTTGTAATGGGATGATGATGAAGAGAGAATACAGG  
GGTCAGCGATCAGTGAAAGCATTGGCAGATTACATCAGGC

## FIGURE 128

GCCCACGCGTCCGATGGCGTTCACGTTCGCGGCCCTCTGCTACATGCTGGCGCTGCTGCTCA  
CTGCCCGCCTCATCTTCGCCATTGGCACATTAGCATTGATGAGCTGAAGACTGAT  
TACAAGAACCTATAGACCAGTGTAAATACCCCTGAATCCCCTGTACTCCCAGAGTACCTCAT  
CCACGCTTCTCTGTGTATGTTCTTGCGAGCAGAGTGGCTTACACTGGGTCTCAATA  
TGCCCCTCTGGCATATCATATTGGAGGTATATGAGTAGACCAGTGTAGTGGCCAGGA  
CTCTATGACCTACAACCATCATGAATGCAGATATTCTAGCATATTGTCAAAGGAAGGATG  
GTGCAAATTAGCTTTATCTTAGCATTCTTACTACCTATATGGCATGATCTATGTT  
TGGTGAGCTTTAGAACAACACAGAAGAATTGGTCCAGTTAAGTGCATGCAAAAGCCAC  
CAAATGAAGGGATTCTATCCAGCAAGATCCTGTCCAAGAGTAGCCTGTGGAATCTGATCAGT  
TACCTTAAAAATGACTCCTTATTTTAAATGTTCCACATTTGCTGTGAAAGACTG  
TTTCATATGTTACTCAGATAAAGATTTAAATGGTATTACGTATAAATTAAATATAAAAT  
GATTACCTCTGGTGTGACAGGTTGAACTTGCACTTCTTAAGGAACAGCCATAATCCTCTG  
AATGATGCATTAATTACTGACTGTCCTAGTACATTGAAAGCTTGTATAGGAACATTGTA  
GGGCTCATTGGTTTCATTGAAACAGTATCTAATTATAAATTAGCTGTAGATATCAGGTGC  
TTCTGATGAAGTGAATGTATCTGACTAGTGGAAACTTCATGGGTTCTCATCTGTC  
ATGTCGATGATTATATGGATACATTACAAAAATAAAAGCGGAAATTCCCTCGCTT  
GAATATTATCCCTGTATATTGATGAATGAGAGATTCCCATATTCCATCAGAGTAATAAA  
TATACTTGCTTAATTCTTAAGCATAAGTAAACATGATATAAAATATGCTGAATTACTT  
GTGAAGAATGCATTTAAAGCTATTTAAATGTGTTTATTGTAAGACATTACTTATTAAG  
AAATTGGTTATTATGCTTACTGTTCTAATCTGGTGGTAAAGGTATTCTTAAGAATTGCAAGG  
TACTACAGATTTCAAAACTGAATGAGAGAAAATTGTATAACCATCCTGCTGTTCTTAGT  
GCAATACAATAAAACTCTGAAATTAAAGACTC

## FIGURE 129

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA23330
<subunit 1 of 1, 144 aa, 1 stop
<MW: 16699, pI: 5.60, NX(S/T): 0
MAFTFAAFCYMLALLTAALIFFAIWHIIAFDELKTDYKNPIDQCTLNPLVLPEYLIHAFF
CVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGWCKLA
FYLLAFFYYLYGMIYVLVSS
```

**Important features:**

**Signal peptide:**

amino acids 1-20

**Type II transmembrane domain:**

amino acids 11-31

**Other transmembrane domain:**

amino acids 57-77 and 123-143

## **FIGURE 130**

ATTATAGCATTGATGAGCTGAAGACTGATTACAAGATCCTATAGACCAGTGTAAATACCTG  
AATCCCCTTGTACTCCCAGAGTACCTCATCCACGCTTCTGTGTATGTTCTTGTC  
AGCAGAGTGGCTTACACTGGGTCTCAATATGCCCTCTGGCATATCATATTGGAGGTATA  
TGAGTAGACCAGTGTGAGTGGCCCAGGACTCTATGACCCCTACAACCACATGAATGCAGAT  
ATTCTAGCATATTGTCAGAAGGAAGGATGGTCAAATTAGCTTTATCTCTAGCATT  
TTACTACCTATATGGCATGATCTATGTTTGGTGAGCTCTAGAACACACAGAAGAATT  
GGTCCAGTTAAGTGCATGCAAAAGCCACCAATGAAGGGATTCTATCCAGCAAGATCCTGT  
CCAAGAGTAGCCTGTGGAATCTGATCAGTTACTTAAAAAATG

## FIGURE 131

CGGACGCGTGGGGAAACCCTCCGAGAAAACAGCAACAAGCTGAGCTGCTGTGACAGAGGG  
GAACAAGATGGCGCGCCGAAGGGAGCCTCTGGGTGAGGACCCAACTGGGCCTCCGCCGC  
TGCTGCTGCTGACCATGGCCTGGCCGGAGGTTGGGACCGCTCGGCTGAAGCATTGAC  
TCGGTCTTGGGTGATAACGGCGTCTGCCACCGGGCCTGTCAGTTGACCTACCCCTGCACAC  
CTACCCCTAAGGAAGAGGGAGTTGTACGCATGTCAGAGAGGTTGCAGGCTGTTCAATTGTC  
AGTTTGTGGATGATGGAATTGACTAAATCGAACTAAATTGGAATGTGAATCTGCATGTACA  
GAAGCATAATTCCAATCTGATGAGCAATATGCTGCCATCTGGGTGCCAGAACAGCTGCC  
ATTGCTGAAC TGAGACAAGAACAACTTATGTCCTGATGCCAAAAATGCACCTACTCTTC  
CTCTAACTCTGGTGAGGT CATTCTGGAGTGACATGATGGACTCCGCACAGAGCTTCATAACC  
TCTTCATGGACTTTTATCTCAAGCCGATGACGGAAAATAGTTATATTCCAGTCTAAGCC  
AGAAATCCAGTACGCACCACATTGGAGCAGGAGCCTACAAATTGAGAGAACATCTCTAA  
GCAAAATGTCCTATCTGCAAATGAGAAATTACAAGCGCACAGGAATTTCTGAAGATGGA  
GAAAGTGATGGCTTTAAGATGCCCTCTCTTAACACTCTGGGTGGATTAACTACAACTCT  
TGTCCTCTGGTGATGGTATTGCTTGGATTGTTGTGCAACTGTTGCTACAGCTGGAGC  
AGTATGTTCCCTCTGAGAAGCTGAGTATCTATGGTACTGGAGTTATGAATGAACAAAAG  
CTAAACAGATATCCAGCTTCTCTTGTTGTTAGATCTAAACTGAAGATCATGAAGA  
AGCAGGGCCTCTACCTACAAAAGTGAATCTGCTCATTCTGAAATTTAAGCATTTC  
AAAAGACAAGTGTAA TAGACATCTAAAATTCCACTCCTCATAGAGCTTTAAAATGGTTCA  
TTGGATATAGGCCTTAAGAAATCACTATAAAATGCAAATAAGTTACTCAAATCTGTG

## FIGURE 132

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA26847
<subunit 1 of 1, 323 aa, 1 stop
<MW: 36223, pI: 5.06, NX(S/T): 1
MAAPKGSLWVRTQLGLPPLLLTMAAGGSGTASAEAFDSVLGDTASCHRACQLTYPLHTYP
KEEELYACQRGCRLFSICQFVDDGIDLNRKLECESACTEAYSQSDEQYACHLGCQNQLPFA
ELRQEQLMSLMPKMHLLFPLTLVRSFWSDMMDSAQSFITSSWTFYLQADDGKIVIFQSKPEI
QYAPHLEQEPNLRESSLSKMSYLQMRNSQAHRNFLEDGESDGFLRCLSLNSGWILTTTLVL
SVMVLLWICCATTAVATEQYVPSEKLSIYGDLEFMNEQKLNRYPASSLVVVRSKTEDHEEAG
PLPTKVNLAHSEI
```

**Important features:**

**Signal peptide:**

amino acids 1-31

**Transmembrane domain:**

amino acids 241-260

**N-glycosylation site.**

amino acids 90-93

## **FIGURE 133**

TTGGGTGATACGGCGTCTGCCACCGGGCCTGTCAGTTGACCTACCCCTGCACACCTACCC  
TAAGGAAGAGGAGTTGTACGCATGTCAGAGAGGTTGCAGGCTGTTCAATTGTCAGTTG  
TGGATGATGGAATTGACTTAAATCGAACTAAATTGGAATGTAATCTGCATGTACAGAAGCA  
TATTCCAATCTGATGAGCAATATGCTTGCCATCTTGGTTGCCAGAACATCAGCTGCCATTGCG  
TGAACGTGAGACAAGAACAACTTATGTCCCTGATGCCAAAAATGCACCTACTCTTCCTCTAA  
CTCTGGTGAGGTCAATTCTGGAGTGACATGATGGACTCCGC

## FIGURE 134

CACACTGGCCGGATCTTTAGAGTCCTTGACCTGACCAAGGGTCNGGAAAACAGCAACAA  
GCTGAGCTGCTGTGACAGAGGAACAAGATGGCGCGCCGAAGGGAGCCTTGGGTGAGGAC  
CCAACGGGGCTCCCGCGCTGCTGCTGACCATGGCCTGGCGAGGTTGGGGACCG  
CTTCGGCTGAAGCATTGACTCGGTCTGGTGATACGGCGTCTGCCACCAGGGCTGTCAG  
TTGACCTACCCCTTGACACCTACCCCTAACGAAAGAGGAGTTGTACGCATGTCAGAGAGGTTG  
CAGGCTGTTTCAATTGTCAGTTGGATGATGGAATTGACTTAAATCGAACTAAATTGG  
AATGTGAATCTGCATGTACAGAACATATTCCCAATCTGATGAGCAATATGCTTGCCATCTT  
GGTGCAGAACATCAGCTGCCATTGCTGAACGTGAGACAAGAACAACTTATGTCCCTGATGCC  
AAAAATGCACCTACTCTTCCTCTAACTCTGGTGAGGTATTCTGGAGTGACATGATGGACT  
CCGC

## FIGURE 135

GCGAGGTGGCGATCGCTGAGAGGCAGGAGGGCCGAGGCCGGCCTGGGAGGCAGGCCGGAGGT  
GGGGCGCCGCTGGGCCGGCCGCACGGCTTCATCTGAGGGCGCACGCCCGGACCGAGC  
GTGCGGACTGGCCTCCCAAGCGTGGGCGACAAGCTGCCGGAGCTGCAATGGCCGGCTG  
GGGATTCTTGGCCTCCTGGCGCGTGTGGCTGCTCAGCTGGCCACGGAGAGGAGC  
AGCCCCCGGAGACAGCGGCACAGAGGTGCTCTGCCAGTTAGTGGTTACTTGGATGATTGT  
ACCTGTGATGTTGAAACCATTGATAGATTTAATAACTACAGGCTTCCCAGACTACAAAAA  
ACTTCTTGAAAGTGACTIONTAGGTATTACAAGGTAAACCTGAAGAGGCCGTGTCCTTCT  
GGAATGACATCAGCCAGTGTGGAAGAAGGGACTGTGCTGTCAAACCATGTCATCTGATGAA  
GTTCCTGATGGAATTAAATCTGCGAGCTACAAGTATTCTGAAGAACCAATAATCTCATTGA  
AGAATGTGAACAAGCTGAACGACTTGGAGCAGTGGATGAATCTCTGAGTGAGGAAACACAGA  
AGGCTGTTCTCAGTGGACCAAGCATGATGATTCTCAGATAACTCTGTGAAGCTGATGAC  
ATTCACTCCCCTGAAGCTGAATATGTAGATTGCTTCTTAATCCTGAGCGCTACACTGGTTA  
CAAGGGACCAGATGCTTGGAAAATATGGAATGTCATCTACGAAGAAAATGTTAACGCCAC  
AGACAATTAAAAGACCTTAAATCCTTGGCTCTGGTCAAGGGACAAGTGAAGAGAACACT  
TTTACAGTTGGCTAGAAGGTCTCTGTGTAGAAAAAAAGAGCATTCTACAGACTTATATCTGG  
CCTACATGCAAGCATTAAATGTGCATTGAGTGAAGATATCTTACAAGAGACCTGGTTAG  
AAAAGAAATGGGGACACAACATTACAGAATTCAACAGCGATTGATGAAATTGACTGAA  
GGAGAAGGTCCAAGAAGGCTTAAGAACCTGTATTTCTACTTAATAGAACTAAGGGCTT  
ATCCAAAGTGTACCATTCTCGAGCGCCAGATTCAACTCTTACTGGAAATAAAATTC  
AGGATGAGGAAAACAAATGTTACTTCTGGAAATACTTCATGAAATCAAGTCATTCCCTTG  
CATTGATGAGAATTCACTTGTGGGATAAAAAGAAGCACACAAACTAAAGGAGGA  
CTTCTGACTGCATTAGAAATATTCAAGAATTATGGATTGTGGTTGTTAAATGTC  
GTCTGTGGGAAAGCTTCAGACTCAGGGTTGGGCACTGCTCTGAAGATCTTATTTCTGAG  
AAATTGATAGCAAATATGCCAGAAAGTGGACCTAGTTATGAATTCCATCTAACAGACAAGA  
AATAGTATCATTATTCAACGCATTGGAAGAATTCTACAAGTGTGAAAGAATTAGAAAATC  
TCAGGAACCTGTTACAGAAATTCATAAAGAAAACAAGCTGATATGTGCTGTTCTGGAC  
AATGGAGGCAGAAAGAGTGGATTTCATTCAAAGGCATAATAGCAATGACAGTCTTAAGCCAA  
ACATTATATAAAGTTGCTTGTAAAGGAGAATTATATTGTTAAAGTAAACACATT  
AAAAATTGTGTTAAGTCTATGTATAACTACTGTGAGTAAAGTAATACTTAAATAATGTG  
GTACAAATTAAAGTTAAATTGAATAAAAGGAGGATTATCAAATTAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 136**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53974  
<subunit 1 of 1, 468 aa, 1 stop  
<MW: 54393, pI: 5.63, NX(S/T): 2  
MGRGWGFLFGLLGAWLSSGHGEEQPETAAQRCFCQVSGYLDCTCDVETIDRFNNYRLF  
PRIQLLESDYFRYYKVNLKRCPFWNDISQCGRRDCAVKPCQSDEVPDGIKSASYKYSEE  
NNLIEECEQAERLGAVDESLSEETQKAVLQWTKHDDSSDNFCEADDIQSPEAEYVDLLNPE  
RYTGYKGPAWKIWNVIYEENCFKPQTIKRPLNPLASGQGTSEENTFYSWLEGLCVEKRAFY  
RLISGLHASINVHLSARYLLQETWLEKKWGNITEFQQRFDGILTEGEGPRLKNLYFLYLI  
ELRALSKVLPFFERPFDQLFTGNKIQDEENKMLLEILHEIKSFPFHFDENSFFAGDKKEAH  
KLKEDFRLHFRNISRIMDCVGCFKCRWGKLQTQGLGTALKILFSEKLIANMPESGPSYEFH  
LTRQEIVSLFNAFGRISTSVKELENFRNLLQNIH

**Important features:**

**Signal peptide:**

amino acids 1-23

**N-glycosylation site.**

amino acids 280-283 and 384-387

**Amidation site.**

amino acids 94-97

**Glycosaminoglycan attachment site.**

amino acids 20-23 and 223-226

**Aminotransferases class-V pyridoxal-phosphate**

amino acids 216-222

**Interleukin-7 proteins**

amino acids 338-343

## **FIGURE 137**

GCTGGAAATATGGATGTCATCTACGAGAAACTGTTTAAGCCACAGACAATTAAAAGACCTT  
TAAATCCTTGGCTCTGGTCAAGGGACAAGTGAAGAGNACACTTTACAGTGGCTAGAA  
GGTCTCTGTGTAGAAAAAAGAGCATTCTACAGACTTATCTGGCCTACATGCAAGCATTAA  
TGTGCATTTGAGTGCAAGATATCTTTACAAGAGACCTGGTTAGAAAAGAAATGGGACACA  
ACATTACAGAATTNAACAGCGATTGATGGAATTTGACTGAAGGAGAAGGTCCAAGAAGG  
CTTAAGAACCTGTATTTCTACTTAATAGAACTAAGGGCTTATCCAAAGTGTACCATT  
CTTNGAGCGCCCAGATTTCAACTNTTACTGGAAATAAAATTCAAGGATGAGGNAACAAAA  
TGTTACTTTGGAAATACTTCATGAAATCAAGTCATTCCTTGCAATTGATGAGAATTCA  
TTTTTTGCTG

## FIGURE 138

CGGACGCGTGGCGGACGCGTGGCGGACGCGTGGTTGGAGGGGCAGGATGGGAGGGAA  
AGTGAAGAAAACAGAAAAGGAGAGGGACAGAGGCCAGAGGACTCTCATACTGGACAGAAC  
CGATCAGGCATGGACTCCCCTCGTCACTCACCTGTTGCCCCGTGTTCTGACAGG  
TCTCTGCTCCCCTTAACCTGGATGAACATCACCCACGCCTATTCCCAGGGCCACCAGAAG  
CTGAATTGGATACAGTGTCTAACACATGTTGGGGTGGACAGCGATGGATGCTGGTGGC  
GCCCCCTGGATGGGCCTTCAGGCGACCGGAGGGGGACGTTATCGCTGCCCTGTAGGGGG  
GGCCCACAATGCCCATGTGCCAAGGGCCACTTAGGTGACTACCAACTGGAAATTCATCTC  
ATCCTGCTGTGAATATGCACCTGGGATGTCTCTGTTAGAGACAGATGGTGATGGGGATTC  
ATGGTGAGCTAAGGAGAGGGTGGCAGTGTCTGAAGGTCCATAAAAGAAAAAGAGAA  
GTGTGGTAAGGGAAAATGGTCTGTGTGGAGGGTCAAGGAGTTAAAACCCTAGAAAGCAA  
AGGTAGGTAATGTCAGGGAGTAGTCTTCATGCCTCCTTCAACTGGGAGCATGTTCTGAGGGT  
GCCCTCCCAAGCCTGGAGTAACTATTTCCCCCATCCCCAGGCCGTGCCCTCTTGGTCT  
CGTGCTTGTGGCAGCTGTCTTCAGTTCTGGATATGTGCCGTGGATGCTTCATTCCA  
GCCTCAGGGAAGCCGGCACCCACTGCCAACGTGAGCCAGAGGAAGGCTGAGTACTTGGTT  
CCCAGAAGGAGATACTGGTGGAAAAGATGGGCAAAGCGGTATGATGCCTGGCAAAGGG  
CCTGCATGGCTATCCTCATTGCTACCTAACGTGCTTGCAAAGCTCCATTTGGGAGGCCAAG  
TTCAGACTCCTGGCCAGGTGTGGTGGCCACACCTGTAATTCTAGCACTTGGGAGGCCAAG  
GTGGGCAGATCACTTGAGGTCAGGAGTTCAAGACCAGCCTGGCAACATGGTAAACTCCAT  
CTCTACTAAAAAAAAAATAAAAAATTAGCTGGGTGCGCTAGTGCATGCCTGTAATCTC  
ATCTACTCGGGAGGCTAAGACAGGAGACTCTCACTTCAACCCAGGAGGTGGAGGTTGCGGTG  
AGCCAAAGATTGTGCCTCTGCACTCTAGCGTGGGTGACAGAGTAAGCGAGACTCCATCTCAA  
AATAATAATAATAATTCAGACTCCTTATCAGGAGTCCATGATCTGGCCTGGCACAGTAA  
CTCATGCCTGTAATCCAACATTTGGGAGGCCAACGCCAGGAGGATTGCTGAGGTCTGGAG  
GTTTGAGACCAGCCTGGCAACATAGAAAGACCCATCTAAATAATGTTTAAAAAT

## **FIGURE 139**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57039
><subunit 1 of 1, 124 aa, 1 stop
><MW: 13352, pI: 5.99, NX(S/T): 1
MELPFVTHLFLPLVFLTGLCSPFNLDHHPRLFPGPPEAEFGYSVLQHVGGGQRWMLVGAPW
DGP SGD RRG DVY RCP VGG AHN APC AKG HLG DY QLG NSH PAV NMHL GMS LLE TDG DGG F MVS
```

**Important features:**

**Signal peptide:**

amino acids 1-22

**Cell attachment sequence.**

amino acids 70-73

**N-glycosylation site.**

amino acids 98-101

**Integrins alpha chain proteins**

amino acids 67-81

## FIGURE 140

CACAGTTCCCCACCATCACTCNCNTCCCATTCTTCCAACTTTATTTTAGCTGCCATTGGGA  
GGGGGCAGGATGGGAGGGAAAGTGAAGAAAACAGAAAAGGAGAGGGACAGAGGCCAGAGGAC  
TTCTCATACTGGACAGAACCGATCAGGCATGGAACCTCCCTTGTCACTCACCTGTTCTTG  
CCCCTGGTGGTCTGACAGGTCTCTGCTCCCCCTTAACCTGGATGAACATCACCCACGCCT  
ATTCCCAGGGCCACCAGAAGCTGAATTGGATAACAGTGTCTTACAACATGTTGGGGGTGGAC  
AGCGATGGATGCTGGTGGCGCCCCCTGGATGGCCTTCAGGCACCGGAGGGGGACGTT  
TATCGCTGCCCTGTAGGGGGGCCACAATGCCCATGTGCCAAGGGCCACTTAGGTGACTA  
CCAACCTGGAAATTCATCTCATCCTGCTGTGAATATGCACCTGGGATGTCTCTGTTAGAGA  
CAGATGGTGATGG

## **FIGURE 141**

AAAGTTACATTTCTCTGGAACTCTCCTAGGCCACTCCCTGCTGATGCAACATCTGGGTTTG  
GGCAGAAAGGAGGGTGCTCGGAGCCGCCCTTCTGAGCTCCTGGGCCGCTCTAGAACAA  
ATT CAGGCTCGCTCGACTCAGACCTCAGCTCCAACATATGCATTCTGAAGAAAGATGGCT  
GAGATGGACAGAATGCTTATTGGAAAGAACAAATGTTCTAGGTCAAACAGTCTACCA  
**AATG**CAGACTTCACAATGGTCTAGAAGAAATCTGGACAAGTCTTTCATGTGGTTTCT  
ACGCATTGATTCCATGTTGCTCACAGATGAAGTGGCCATTCTGCCTGCCCTCAGAACCTC  
TCTGTACTCTCAACCAACATGAAGCATCTCTGATGTGGAGCCCAGTGATCGGCCTGGAGA  
AACAGTGTACTATTCTGTCGAATACCAGGGGAGTACGAGAGCCTGTACAGGCCACATCT  
GGATCCCCAGCAGCTGGTGCTCACTCACTGAAGGTCTGAGTGTGATGTCAGTGACATC  
ACGCCACTGTGCCATACAACCTTCGTGTAGGGCACATTGGGCTCACAGACCTCAGCCTG  
GAGCATCCTGAAGCATCCCTTAATAGAAACTCAACCATTACCGACCTGGGATGGAGA  
TCACCAAAGATGGCTTCCACCTGGTTATTGAGCTGGAGGACCTGGGGCCCAGTTGAGTTC  
CTTGTGGCCTACTGGAGGAGGGAGCCTGGTGCCGAGGAACATGTCAAAATGGTGAGGAGTGG  
GGGTATTCCAGTGCACCTAGAAACCATGGAGCCAGGGCTGCATACTGTGTGAAGGCCAGA  
CATTGTAAGGCCATTGGGAGGTACAGCGCCTCAGCCAGACAGAACATGTGTGGAGGTGCAA  
GGAGAGGCCATTCCCTGGTACTGGCCTGTTGCCTTGTGCTCATGCTGATCCTTGT  
GGTGTGCCACTGTTGTCCTGGAAAATGGGCCGCTGCTCCAGTACTCCTGTTGCCGTGG  
TGGCCTCCCAGACACCTGAAAATAACCAATTCAACCCAGAAGTTAACAGCTGCAGAAGG  
GAGGAGGTGGATGCCGTGACGGCTGTGATGTCTCCTGAGGAACCTCCTCAGGGCTGGAT  
**CTCA****TAG**TTTGCAGAAGGGCCAGGTGAAGCCAGAACCTGGTCTGCATGACATGGAAACC  
ATGAGGGACAAGTTGTTCTGTTTCCGCCACGGACAAGGGATGAGAGAACAGTAGGAAGA  
GCCTGTTCTACAAGTCTAGAACCAACCATCAGAGGAGGGTGGTTGCTAACAGAACAC  
TGACTGAGGCTTAGGGATGTGACCTCTAGACTGGGGCTGCCACTGCTGGCTGAGCAACC  
CTGGAAAAGTGACTTCATCCCTCGGTCTAACAGTTCTCATCTGAATGGGGAATTACC  
TACACACCTGCTAAACACACACACAGACTCTCTCTATATACACACGTACACATAAA  
TACACCCAGCACTGCAAGGCTAGAGGGAAACTGGTGACACTCTACAGTCTGACTGATTGAG  
TGTGTTCTGGAGAGCAGGACATAATGTATGATGAGAACATGATCAAGGACTCTACACACTGGGT  
GGCTTGGAGAGGCCACTTCCAGAATAATCCTTGAGAGAAAAGGAATCATGGAGCAATGG  
TGTGAGTTCACTCAAGCCCAATGCCGTGCAAGAGGGAAATGGCTTAGCGAGCTCTACAGT  
AGGTGACCTGGAGGAAGGTACAGCCACACTGAAAATGGGATGTGCAACACGGAGGATC  
CATGAACTACTGTAAGTGTGACAGTGTGTCACACTGCAGACAGCAGGTGAATGTATGT  
GTGCAATGCGACGAGAACATGCAGAACATGTGCACTGTTGTTGCTCCTTTTC  
TGTGTTGTAAGTACAGAACATTCAAGAAATAAAAGGCCACCTGCCAAAGCGGTAAAAAA  
AAAAAAAAAA

## **FIGURE 142**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57033
<subunit 1 of 1, 311 aa, 1 stop
<MW: 35076, pI: 5.04, NX(S/T): 2
MQTFTMVLLEIWTSLFMWFFYALIPCLLTDEVAILPAPQNLSQLSTNMKHLLMWSPIAPGE
TVYYSVEYQGEYESLYTSHIWIPSSWCSLTEGPECDVTDDITATVPYNLRVRATLGSQTSAW
SILKHPFNRNSTILTRPGMEITKDGFLVIELEDLGPFQFEFLVAYWRREPGAEHVKMVRSG
GIPVHLETMEPGAAYCVKAQTFVKAIGRYSAFSQTECVEVQGEAIPLVLALFAFGFMLLILV
VVPLFVWKMGRLLQYS CCPVVVLPTDLKITNSPQKLISCRREEVDACATAVMSPEELLRAWIS
```

**Important features:**

**Signal peptide:**

amino acids 1-29

**Transmembrane domain:**

amino acids 230-255

**N-glycosylation site.**

amino acids 40-43 and 134-137

**Tissue factor proteins.**

amino acids 92-119

**Integrins alpha chain proteins**

amino acids 232-262

## **FIGURE 143**

TCCTGCTGATGCACATCTGGTTGGAAAAGGAGGTTGCTCGAGCCGCCCTTAGCTT  
CCTGGCCGGCTCTAGAACAAATTCAAGGCTCGCTGCGACTAGACCTCAGCTCCAACATATGCA  
TTCTGAAGAAAGATGGCTGAGATGACAGAATGCTTATTTGAAAGAAACAATGTTCTAGG  
TCAAACGTGAGTCTACCAAATGCAGACTTCACAATGGTTCTAGAAGAAATCTGGACAAGTCT  
TTTCATGTGGTTTCTACGCATTGATTCCATGTTGCTCACAGATGAAGTGGCCATTCTGC  
CTGCCCTCAGAACCTCTGTACTCTCAACCAACATGAAGCATCTCTGATGTGGAGGCCA  
GTGATCGCGCCTGGAGAACAGTGTACTATTCTGTAATACCAGGGGAGTACGAGAGCCT  
GTACACGAGCCACATCTGGATCCCCAGCAGCTGGTGCTCACTCACTGAAGGTCTGAGTGTG  
ATGTCACTGATGACATCACGCCACTGTGCCATACAACCTTGTGTCAGGCCACATTGGC  
TCACAGACCTCAGCCTGGAGCATCCTGAAGCATCCCTTAATAGAAACTCAACCATCCTTAC  
CCGACCTGGATGGAGATCACAAAGATGGCTNCACCTGGTTATTGAGCTGGAGGACCTGG  
GGCCCCAGTTGAGTTCCCTGGCCTANTGGAGGAGGGCGAACCCCTGCGCGCAAGGG  
GTTNGCGAACCCCTTGCAGCCGCTGGGTATCTCTCGAGAAAAGAGAGGCCAATATGACCC  
ACATACTCAATATGGACGAANTGCTATTGTCCACCTGTTGAGTGGCGCTGGTTGAT

## FIGURE 144

CCCACGCGTCCGCCACCGTCCGAGGGACAAGAGAGAAGAGAGACTGAAACAGGGAGAAGA  
GGCAGGAGAGGAGGAGGTGGGGAGAGCACGAAGCTGGAGGCCGACACTGAGGGAGGGCGGG  
GGAGGTGAAGAAGGAGAGAGGGAGAAGAGGCAGGAGCTGGAAAGGAGAGAGGGAGGAGGAG  
GAGGAGATGCCGGATGGAGACCTGGAGTTAGGTGGCTTGGAGAGCTTAATGAAAAGAGAAC  
GGAGAGGAGGTGTGGGTTAGAACCAAGAGGTAGCCCTGTGGCAGCAGAAGGCTGAGAGGA  
GTAGGAAGATCAGGAGCTAGAGGGAGACTGGAGGGTTCCGGAAAAGAGCAGAGGAAAGAGG  
AAAGACACAGAGAGACGGGAGAGAGAAGAAGAGTGGTTGAAGGGCGGATCTCAGTCCCTG  
GCTGCTTGGCATTGGGAACTGGGACTCCCTGTGGGAGGAGAGGAAAGCTGGAAGTCCT  
GGAGGGACAGGGTCCCAGAAGGAGGGACAGAGGAGCTGAGAGAGGGGGCAGGGCGTTGG  
CAGGGTCCCTCGGAGGCCTGGGATGGGGCTGCAGCTCGTCTGAGCGCCCTCGAGC  
GCTGGTACTCTGGCTGCACTGGGGCAGCAGCTCACATCGGACCAGCACCTGACCCGAGG  
ACTGGTGGAGCTACAAGGATAATCTCCAGGGAAACTCGTGCAGGGCTCCTTCTGGGC  
CTGGTGAATGCAGCGTGGAGTCTGTGTGCTGTGGGAAGCGGCAGAGCCCCGTGGATGTGGA  
GCTGAAGAGGGTTCTTATGACCCCTTCTGCCCTTAAGGCTCAGCAGTGGAGGAGAGA  
AGCTCCGGGAACCTGTACAACACCGGCCGACATGTCTCCTGCCTGCACCCGACCT  
GTGGTCAATGTGTCTGGAGGTCCCCTCCTTACAGCCACCGACTCAGTGAACCGCCTGCT  
GTTGGAGCTCGCGACGGAGCCGGCTCGAACATCAGATCAACCACCAAGGGCTCTGCTG  
AGGTGCAGCTCATTCACTCAACCAGGAACCTACGGGAATTCAAGCAGTGCCTCCCGGG  
CCCAATGGCCTGGCATTCTCAGCCTCTTGTCAACGTTGCCAGTACCTCTAACCCATTCT  
CAGTCGCCTCCTTAACCGCGACACCCTCACTCGCATCTCCTACAAGAATGATGCCTACTT  
TTCAAGACCTGAGCCTGGAGCTCCTGTTCCCTGAATCCTCGGCTCATCACCTATCAGGC  
TCTCTCAGCACCCGCCCTGCTCCGAGACTGTCACCTGGATCCTCATTGACCGGGCCCTCAA  
TATCACCTCCCTCAGATGCACCTCGAGACTCCTGAGCCAGAATCCTCCATCTCAGATCT  
TCCAGAGCCTCAGCGGTAAACAGCCGGCCCTGCAGCCCTGGCCACAGGGCACTGAGGG  
AACAGGGACCCCGGCACCCCGAGAGGGCGCTGCCAGGGCCAACTACCGCCTGCATGTGGA  
TGGTGTCCCCATGGTCGCTGA~~G~~ACTCCCCCTCGAGGATTGCACCCGCCGCTTAAGCCTC  
CCCACAAGGCGAGGGAGTTACCCCTAAAACAAAGCTATTAAAGGGACAGAATACTTA

## **FIGURE 145**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA34353
<subunit 1 of 1, 328 aa, 1 stop
<MW: 36238, pI: 9.90, NX(S/T): 3
MGAAARLSAPRALVLWAALGAAAHHGPAPDPEDWWSYKDNLQGNFVPGPPFWGLVNAAWSLC
AVGKRQSPVDVELKRVLYDPFLPPLRLSTGGEKLRGTLYNTGRHVSFLPAPRPVVNVSGGPL
LYSHRLSELRLLGARDGAGSEHQINHQGFSAEVQLIHFNQELYGNFSAASRGPNGLAILSL
FVNVAESTSNPFLSRLLNRTDTITRISYKNDAYFLQDLSLELLFPESFGFITYQGSLSTPPCSE
TVTWILIDRALNITSLQMHSRLLSQNPPSQIFQSLSGNSRPLQPLAHRALRGNRDPRHPER
RCRGPNYRLHVDGVPHGR
```

**Important features:**

**Signal peptide:**

amino acids 1-23

**Transmembrane domain:**

amino acids 177-199

**N-glycosylation site.**

amino acids 118-121, 170-173 and 260-263

**Eukaryotic-type carbonic anhydrases proteins**

amino acids 222-270, 128-164 and 45-92

## **FIGURE 146**

GGCGCCTGGTCTGCGCTACTGGCTGTACGGAGCAGGAGCAAGAGGTCGCCGCCAGCCTCCGCCAGCCTC  
GTTCGTGTCCCCGCCCTCGCTCCTGCAGCTACTGCTCAGAACGCTGGGGGCCACCCCTGGCAGACTAACGAA  
GCAGCTCCCTCCCACCCAAC TGCAAGGCTTAATTGGACGCTTGCCCTTCTCCAGGTTGAGGGAGC  
CGCAGAGGCGAGGCTCGGTATTCTGCAGTCAGCACCCACGTCGCCGCCAGCCTCGGTGCTCAGGCCCTTC  
GCGAGCGGGCTCTCGCTCGGTTCCCTGTGAAGGCTCTGGCGCTGCAGAGGCCGTCGGTTGGCT  
CACCTCTCCCAGGAAACTCACA CACTGGAGAGC AAAAGGAGTGGAAAGAGCCTGTTGGAGATTTCTGGGAA  
ATCC TGAGGTCA TT TGAAGTGTACCGCGGGAGTGGCTCAGAGTAACCACAGTGCTGTTCATGGCTAGA  
GCAATTCCAGCCATGGTGGTCCCAATGCCACTTTATTGGAGAAAATTTGGAAAAATACATGGATGAGGATGGT  
GAGTGGTGGATAGCCAAAACAGAGGAAAAGGGCATCACAGACAATGACATGCCAGAGTATTTGGACCTTCAT  
AATAAATTACGAAGTCAGGTGTATCCAACAGCCTTAATATGGAGTATATGACATGGATGTAGAGCTGGAAAGA  
TCTCGAGAATCTGGGCTGAAAGTTGCTGTGGAACATGGACCTGCAAGCTGCTTCCATCAATTGGACAGAAT  
TTGGGAGCACACTGGGGAAAGATATA GGCCCCGACGTTCATGTACAATCGTGGTATGATGAAAGACTTT  
AGCTACCCATATGAACATGAATGCAACCCATATTGTCATTAGGTGTTCTGGCCCTGTATGTACACATTATACA  
CAGGTCGTGTGGCAACTAGTAACAGAACGTTGTGCCATTAAATTGTGTCAATAACATGAACATCTGGGGCAG  
ATATGGCCCAAAGCTGTCTACCTGGTGTGCAATTACTCCCAAAGGAAACTGGTGGGCCATGCCCTTACAAA  
CATGGGCGGCCCTGTTCTGCCACCTAGTTGGAGGGGCTGTAGAGAAAATCTGTGCTACAAAGAAGGG  
TCAGACAGGTATTATCCCCCTCGAGAAGAGGAAACAAATGAAATAGAACGACAGCAGTCACAGTCCATGACACC  
CATGTCGGACAAGATCAGATGATACTAGCAGAAATGAAGTCATAAGCGCACAGCAAATGTCCTAAATTGTTCT  
TGTGAAGTAAGATTAAGAGATCAGTGCAGGAAACAACCTGCAATTAGGTACGAATGTCCTGCTGGCTTTGGAT  
AGTAAGCTAAAGTTATTGGCAGTGTACATTATGAAATGCAATTCCAGCATCTGTAGAGCTGCAATTCTATTGGT  
ATAATAGACAATGATGGTGGCTGGTAGATATCACTAGACAAGGAAGAACAGCATTATTTCATCAAGTCCAATAGA  
AATGGTATTCAAACAATTGGCAAATATCAGTCTGTAATTCTTCAGTCTCTAAAGTAACAGTTCAAGGCTGTG  
ACTTGTGAAACAACTGTGGAACAGCTCTGTCATTCTATAAGCCTGTTCACATTGCCAACAGGTATACTGTCCT  
CGTAACTGTATGCAAGCAAATCCACATTATGCTCGTGTAAATTGGAAACTCGAGTTATTCTGATCTGTCAGTATC  
TGCAGAGCAGCAGTACATGCTGGAGTGGTCAAAATCACGGTGGTTATGTTGATGTAATGCCGTGGACAAAAGA  
AAGACCTACATTGCTTCTTTCAGAATGGAATTCTCAGAAAGTTACAGAACCTCCAGGAGGAAGGCATT  
AGAGTGGTGTGTTG TGAAACTGAATACTTGGAGAGGACCATAAGACTATTCCAAATGCAATTCTGA  
ATTGGTATAAAACTGTAACATTACTGTACAGAGTACATCAACTATTTCAGCCAAAAGGTGCCAAATGCATA  
TAAATCTGATAAAACAAAGTCTATAAAATAAAACATGGGACATTAGCTTGGAAAAGTAATGAAAATATAATGG  
TTTAGAAATCCTGTGTTAAATATTGCTATATTCTTAGCAGTTATTCTACAGTTAATTACATAGTCATGATT  
GTTCTACGTTCATATATTATGGTGCTTGTATATGCCACTAATAAAATGAATCTAAACATTGAATGTGAATG  
GCCCTCAGAAAATCATCTAGTCATTAAAATAATCGACTCTAAACTGAAAGAACCTTATCACATTTC  
AGTTCAATGCTATGCCATTACCAACTCCAAATAATCTCAAATAATTCCACTTAATAACTGAAAGTTTTTC  
TGTTAATTAGGCATATAGAATATTAAATTCTGATATTGCACTTCTTATTAAATAATCCTTTAATATC  
CAAATGAATCTGTTAAATGTTGATTCTGGGAATGGCTTAAAATAAAATGTAATAAAAGTCAGAGTGGTGGT  
ATGAAAACATTCTAGTGTATGTAAGTAAATGTTAGGGTTAAGCATGGACAGCCAGAGCTTCTATGTACTGTTA  
AAATTGAGGTCACTATTCTTCTGGTATCTGGCAAATACTCCTGCAGGCCAGGAAGTATAATGAAAGAAGTT  
GAACAAAGATGAACTAATGTTAGTACCTATAATGGTGTATATTGTTCTATGAAAATGTTAGCTGCTTGTAA  
ATATTGCCATATCATGGTACCTATAATGGTGTATATTGTTCTATGAAAATGTTAGCTGCTTGTAA  
AATCTGTTAAATGTTAGTCTGGTAAATTCTGCTGGTGGATTACATATTAAATTCTGCTGGTGG  
TAAACATTAAATTAATCATGTTCAAAAAAA

## FIGURE 147

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45417
<subunit 1 of 1, 500 aa, 1 stop
<MW: 56888, pI: 8.53, NX(S/T): 2
MKCTAREWLRTTVLFMARAI PAMVVPNATLLEKLLEKYMDEDGEWWIAKQRGKRAITDNDM
QSILDHLNKLRSQVYPTASNMEYMTWDVELERSAESWAESCLWEHGPASLLPSIGQNLGAHW
GRYRPPTFHVQSWYDEVKDFSYPYEHECNPYCPFRCSGPVCTHYTQVVWATSNRIGCAINLC
HNMMNIWGQIWPKAVYLVNCNYS PKGNWWGHAPYKHGRPCSACPPSFGGGCRENLCYKEGSDRY
YPPREEETNEIERQQSQVHDTHVRTRSSRNEVISAQQMSQIVSCEVRLRDQCKGTTCNR
YECPAGCLDSKAKVIGSVHYEMQSSICRAAIHYGIIDNDGGWVDITRQGRKHYFIKSNRNGI
QTIGKYQSANSFTVSKTVQAVTCETTVEQLCPFHKPASHCPRVYCPRNCMQANPHYARVIG
TRVYSDLSSI CRAAVHAGVVRNHGGYDVMPVDKRKYIASFQNGIFSESLQNPPGGKAFRV
FAVV
```

**Important features:**

**Signal peptide:**

amino acids 1-20

**Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 protein**

amino acids 165-186, 196-218, 134-146, 96-108 and 58-77

**N-glycosylation site**

amino acids 28-31

## **FIGURE 148**

GC GGAGACAAGCGCAGAGCGCAGCGCACGCCACAGACAGCCCTGGCATCCACCGACGGCG  
CAGCCGGAGCCAGCAGAGCCGAAGGCGCCCCGGCAGAGAAAGCCGAGCAGAGCTGGGT  
GGCGTCTCCGGCCGCCGCTCCGACGGGCCAGGCCCTCCCCATGTCCCTGCTCCCACGCCG  
CGCCCTCCGGTCAGCATGAGGCTCCTGGCGCGCTGCTCCTGCTGCTGGCGCTGT  
ACACCGCGCGTGTGGACGGGTCAAATGCAAGTGCTCCCGAAGGGACCCAAAGATCCGCTAC  
AGCGACGTGAAGAACGCTGGAAATGAAGCCAAAGTACCCGACTGCGAGGAGAACGATGGTTAT  
CATCACCAAGAGCGTGTCCAGGTACCGAGGTCAAGGAGCACTGCCTGCACCCAAAGCTGC  
AGAGCACCAAGCGCTTCATCAAGTGGTACAACGCCCTGGAACGAGAACGCGAGGGTCTACGAA  
GAATAGGGTAAAAAACCTCAGAAGGGAAAACTCCAACCAACAGTTGGGAGACTTGTGCAAAGGA  
CTTTCAGATTAAAGCCTTTC  
TTTCTCACAGGCATAAGACACAAATTATATTGTTATGAAGCATTACCAACGGTCAG  
TTTTACATTTATAGCTGCGTGCGAAGGCTTCCAGATGGGAGACCCATCTCTCTTGCT  
CCAGACTTCATCACAGGCTGCTTTATCAAAAGGGAAAACTCATGCCTTCCTTTAA  
AAAATGCTTTTGATTTGTCCACGTCACTATACATCTGAGCTTATAAGCGCCCGGA  
GGAACAATGAGCTGGTGGACACATTCAATTGCAGTGTGCTCCATTCTAGCTGGGAAGC  
TTCCGCTTAGAGGTCTGGCCTGGCGCCTCGGCACAGCTGCCACGGCTCTCTGGCTTATGGCG  
GTCACAGCCTCAGTGTGACTCCACAGTGGCCCTGTAGCCGGCAAGCAGGAGCAGGTCTCT  
CTGCATCTGTTCTCTGAGGAACTCAAGTTGGTGCCAGAAAATGTGCTTCATTCCCCCT  
GGTTAATTTTACACACCCTAGGAAACATTCCAAGATCCTGTGATGGCGAGACAAATGATC  
CTTAAAGAAGGTGTGGGTCTTCCAAACCTGAGGATTTCTGAAAGGTTCACAGGTTCAATA  
TTTAATGCTTCAGAACGATGTGAGGTTCCAAACACTGTCAGCAAAACCTTAGGAGAAA  
TAAAAATATGAATACATGCGCAATAACACAGCTACAGACACACATTCTGTTGACAAGGGAA  
AACCTCAAAGCATGTTCTTCCCTCACCAACAGAACATGCAGTACTAAAGCAATATAT  
TTGTGATTCCCCATGTAATTCTCAATGTTAAACAGTGCAGTCCTCTTGAAAGCTAAGAT  
GACCATGCGCCCTTCCCTGTACATATACCCTTAAGAACGCCCCCTCCACACACTGCC  
CAGTATATGCCGCATTGTACTGCTGTGTTATATGCTATGTACATGTCAGAAACCATTAGCAT  
TGCATGCAGGTTCATATTCTTAAGATGGAAAGTAATAAAATATATTGAAATGTA  
AAAAAA

## **FIGURE 149**

MSLLP~~R~~RAPPVSMRLAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKLEMKP~~K~~YPH  
CEEKMVIITTKSVSRYRGQE~~H~~CLHPKLQSTKRFIKWYN~~A~~WNEKRRVYEE

**Signal sequence:**

amino acids 1-34

## **FIGURE 150**

GCCCCAGGGACTGCTATGGCTTCTTGTTCACCCCGGCTGCGTCATGTTAAACTCCAATGTCCTCCTGTG  
GTTAAGTGTCTTGCCATCAAGTCACCCATTGACAGCCAAGCACAGTATCCAGTTGTCAACACAAATTATGG  
CAAATCCGGGCCTAACGAAACACCGTTACCCATGAGATCTTGGGTCAGTGGAGCAGTAATTAGGGTCCCCTA  
TGCCTCACCCCCACTGGAGAGAGCGGTTTAGCCCCAGAACCCCCGTCCTCTGGACTGGCATCGAAATAC  
TACTCAGTTGCTGTGCCCCAGCACCTGGATGAGAGATCCTACTGCATGACATGTCGCCATCTGGTT  
TACCGCCAATTGGATACCTTGATGACCTATGTCAGATCAAATGAAGACTGCCCTACTTAAACATCTACGT  
GCCACGGAAGATGGAGCCAACACAAGAAAAACGCAGATGATAACGAGTAATGACCCTGGTGAAGAGCGAAGA  
TATTGATGATCAGAACAGTAAGAACCGCTATGGCTATATCCATGGGGATCTTACATGGAGGGCACCGCAA  
CATGATTGACGGCAGCATTTGGCAAGCTACGAAACGTCATCGTGTACCACTAACCGTCTGGGAATACT  
AGGGTTTTAAGTACCGGTGACCAGGCAGCAAAAGGCAACTATGGGCTCTGGATCAGATTCAAGCACTGCGGTG  
GATTGAGGAGAATGTGGGAGCCTTGGGGGGACCCAAAGAGAGTGACCATCTTGGCTGGGGCTGGGGCTC  
CTGTGTAGCCTGTTGACCTGTCCTACTCAGAAGGCTCTTCCAGAAGGCCATTCAGAGCGGCACCGC  
CCTGTCAGCTGGCAGTGAACACCAGCCAGTACACTCGGATATTGGCAGACAAGGTCGGCTGCAACAT  
GCTGGACACCAACGGACATGGTAGAATGCGCTGCGGAACAAGAACTACAAGGAGCTCATCCAGCAGACCATCACCC  
GGCACCTACACATAGCCTCGGGCGGTGATGACGGCAGTCATCCCAGACGACCCAGATCCTGATGGA  
GCAAGGCGAGTCCCTCAACTACGACATCATGCTGGCGTCAACCAAGGGAAAGGCCATGAAGTTCGTGGACGGCAT  
CGTGGATAACGAGGACGGTGTGACGCCAACGACTTGTACTCTCCGTGTCACACTCGTGGACAACCTTACGG  
CTACCCCTGAAGGGAAAGACACTTGGGGAGACTATCAAGTTCATGTCACAGACACTGGGCGATAAGGAAAACCC  
GGAGACGGCGGGAAAACCTGGCTCTCTTACTGACCACCCAGTGGGTGGCCCCCGCCGTGGCCGGACCT  
GCACCGCAGTACGGCTCCCCCACCTACTTCTATGCCTCATGTCACAGGAAATGAAAGCCCAGCTG  
GGCAGATTGGCCATGGTAGAGGCCCCATGTCCTGGCATCCCCATGATCGGCTCACCGAGCTTCA  
TTGTAACCTTCCAAGAACGACGTATGCTCAGCGCCGTGGCATGACCTACTGGACGAACCTGCCAAAACACTGG  
TGATCCAATCAACCAGTCCCTCAGGATACCAAGTTCATCACACAAACCCAGCTTGAAGAAGTGGCCTG  
GTCAAGTATAATCCAAGACAGCTATCTGCATATTGGCTTGAACCCAGAGTGAGAGATCACTACCGGGC  
AACGAAAGTGGTTCTGGTTGAACTGTTCTCATTTGACAACACTGAACGAGATATTCAAGTATGTTCAAC  
AACACAAAGGTTCTCACCAGACATGACATCATTTCCATGGCACCCGGCATCTCCGCCAAGATATGGCC  
AACCAAAACGCCAGCAATCACTCCTGCCAACAACTCTAACGGACCTCACAAACAGGGCTGA  
GGACACAACGTCCCTATTGAAACCAACGAGATTATTCCACCGAATTAGTGTACCATTGCCGTGGGGCGTC  
GCTCTCTCCTCAACATTTAGCTTGGCGCTGTACTACAAAAGGACAAGAGGCCATGAGACTCACAG  
GCGCCCCAGTCCCCAGAGAAACACCAAAATGATATGTCACATCCAGAACGAAGAGATCATGTCCTGAGAT  
GAAGCAGCTGGAACACGATCAGAGTGTGAGTCGCTCAGGCACACACTGAGGCTCACCTGCCAGA  
CTACACCCCTACGCTGCCGGTGCAGATGACATCCACTTATGACGCCAACACCATCACCATTGCCGTGGGGCGTC  
CACACTGACGGGATGCAGCTTGCACACTTTAACACCTTCAGTGGAGGACAAAACAGTACAAATTACCCCA  
CGGACATTCCACCACTAGAGTTAGTTGCCCTATTCCCTCTGCCCTACCGCTCAGCAACAT  
AGAAGAGGGAAAGGAAAG  
GACTTAAGACAAAAATGCAAAAGGCACTCATCCCATCCGGCAGACCCCTATGTTGGTGTGTTCCAGTATTAC  
AAGATCAACTTGACCCCTGTGAAATGTGAGAAGTACACATTCTGTAAATAACTGCTTAAAGATCTCTACCA  
CTCCAATCAATTGTTAGTGTGATAGGACATCACATTCAAGGCCCCGGTGTGTTCCAACGTCATGGAAGCAGCT  
GACACTCTGAAACTCAGCCAAGGACACTTGATATTTTAATTACAATGGAAGTTAAACATTCTTGTG  
CACACAATGGATGGCTCCTTAAGTGAAGAAAGAGTCAATGAGATTGCCCAGCACATGGAGCTGTAATCCAG  
AGAGAAGGAAACGTAGAAATTATTAAAAGAATGGACTGTGCGAGCGAAATCTGTACGGTTCTGTGCAAAGAG  
GTGTTTGCCAGCCTGAACTATATTAGAGACTTTGT

## FIGURE 151

MLNSNVLLWLTAIKFTLIDSQAQYPVVNTNYGKIRGLRTPLPNEILGPVEQYLGVPYASP  
PTGERRFQPPEPPSSWTGIRNTTQFAAVCPQHLDERSLLHDMLPIWFTANLDTLMTYVQDQN  
EDCLYLNIYVPTEDGANTKKNADDITSNDRGEDEDIHDQNSKKPVMVYIHGGSYMEGTGNMI  
DGSILASYGNVIVITINYRLGILGFLSTGDQAAKGNYGLLDQIQALRWIEENVGAFGGDPKR  
VTIFGSGAGASCVSLLTLSHYSEGLFQKAIIQSGTALSSWAVNYQPAKYTRILADKVGCNML  
DTTDMVECLRKNKYKELIQQTITPATYHIAFGPVIDGDVI PDDPQILMEQGEFLNYDIMLGV  
NQGEGLKFVDGIVDNEDGVTPNDFDFSVSNFVDNLYGYPEGKDTLRETIKFMYTDWADKENP  
ETRRKTLVALFTDHQWVAPAVAADLHAQYGSPTYFYAFYHHCQSEMKPSWADSAHGDEVPYV  
FGIPMIGPTELFSCNF SKNDVMLS A VVMTYWTNF A KTGDPNQPV QDTKFIHTKP NR FEEVA  
WSKYNPKDQLYLHIGLKPRVRDHYRATKVAFWLELVPHLHN LNEIFQYVSTTKVPPPDMTS  
FPYGTRRSPAKIWPTTKRPAITPANNPKHSKDPHKTGPEDTTVLIETKRDYSTELSVTIAVG  
ASLLFLNILAFAALYYKKDKRRHETHRRPSPQRNTTNDIAHIQNEEIMSLQMKQLEHDHECE  
SLQAHDTLRLTCPPDYTLR RSPDDIPLMTPNTITMIPNTLTGMQPLHTFNTFSGGQN STN  
LPHGHSTTRV

**Signal sequence:**

amino acids 1-24

**Transmembrane domains:**

amino acids 189-204, 675-692

## **FIGURE 152**

GGGAAAG**ATGGCGCGACTCTGGGACCCCTGGGTCTGGCAGCAGTGGCGGCATGTTGT**  
CGGCTCGGGATGGGTCCAGGATGTTACTCCTTCTTGTGGGTCTGGCAGGGCCA  
CAGCAAGTCGGGGCGGGTCAAACGTTGAGTACTGAAACGGGAGCACTCGCTGTCGAAGCC  
CTACCAGGGTGTGGGCACAGGCAGTCCTCACTGTGGAATCTGATGGCAATGCCATGGTGA  
TGACCCAGTATATCCGCCTAACCCAGATATGCAAAGTAAACAGGGTGCCTGTGGAACCGG  
GTGCCATGTTCCCTGAGAGACTGGAGTTGCAAGGTGACTTCAAAATCCATGGACAAGGAAA  
GAAGAATCTGCATGGGATGGCTGGCAATCTGGTACACAAAGGATCGGATGCAGCCAGGGC  
CTGTGTTGAAACATGGACAAATTGTGGGCTGGGAGTATTGTAGACACCTACCCAAAT  
GAGGAGAAGCAGCAAGAGCGGGTATTCCCTACATCTCAGCCATGGTAACAAACGGCTCCCT  
CAGCTATGATCATGAGCGGGATGGCGGCCTACAGAGCTGGGAGGCTGCACAGCATTGTCC  
GCAATCTCATTACGACACCTCCTGGTATTGCTACGTCAAGAGGCATTGACGATAATG  
ATGGATATTGATGGCAAGCATGAGTGGAGGGACTGCATTGAAGTGCCGGAGTCCGCCGTGCC  
CCGGGCTACTACTTCGGCACCTCCTCCATCACTGGGATCTCTCAGATAATCATGATGTCA  
TTTCTTGAAGTTGTTGAACGTGACAGTGGAGAGAACCCCAGAAGAGGAAAAGCTCCATCGA  
GATGTGTTCTGCCCTCAGTGGACAATATGAAGCTGCTGAGATGACAGCTCCACTGCCGCC  
CCTGAGTGGCCTGCCCTCTCCTCATCGTCTTTCTCCCTGGTGTGTTCTGTATTGCCA  
TAGTCATTGGTATCATACTCTACAACAAATGGCAGGAACAGAGCCAAAGCGCTCTACT**TGA**  
GCCCTCCTGCTGCCACCACTTTGTGACTGTCACCCATGAGGTATGGAAGGAGCAGGCACTG  
GCCTGAGCATGCAGCCTGGAGAGTGTCTCTAGCAGCTGGTGGGACTATATTCTG  
TCACTGGAGTTTGAATGCAGGGACCCCGCATTCCATGGTGTGCATGGGACATCTAATC  
CTGGTCTGGGAAGCCACCCACCCAGGGCAATGCTGCTGATGTCCTTCCCTGCAGTCC  
TTCCATGTGGAGCAGAGGTGTGAAGAGAATTACGTGGTGTGACTCAGAAGGCCCTCTACTCAGTTTG  
AATCCACAAAGAATTAAAAACTGGTAACACCACAGGCTTCTGACCATCCATTGTTGGGTT  
TTGCATTGACCAACCCCTGCCTACCTGAGGAGCTTCTTGAAACCAGGATGGAAACT  
TCTCCCTGCCCTACCTCCTTCACTCCATTGTCCTCTGTGTGCAACCTGAGCTG  
GGAAAGGCATTGGATGCCTCTGTGGGGCTGGGCTGCAGAACACACCTGCGTTCAC  
TGGCCTTCATTAGGTGGCCCTAGGGAGATGGCTTCTGCTTGGATCACTGTTCCCTAGCAT  
GGGTCTGGCTATTGGCATGTCCTCCAAATCAAGTCTCTCAGGCCCTCAGTG  
AAGTTGGCTAAAGGGTGGTGTAAAAATCAAGAGAAGCCTGGAAGACATCATGGATGCCATG  
GATTAGCTGTGCAACTGACCAGCTCAGGTTGATCAAACCAAAAGCAACATTGTCATGTG  
GTCTGACCATGTGGAGATGTTCTGGACTTGCTAGAGCCTGCTTAGCTGCATGTTGTAGT  
TACGATTTGGAAATCCACTTGTAGTGCTGAAAGTGTAAAGGAAGCTTCTTACACCTT  
GGGCTGGATATTGCCAGAGAAGAAATTGGCTTTTTCTTAATGGACAAGAGACAGT  
TGCTGTTCTCATGTTCCAAGTCTGAGAGCAACAGACCCCTCATCATCTGTCCTGGAGAGTT  
CACTGTCATTGAGCAGCACAGCCTGAGTGCTGGCCTCTGTCAACCCATTTCACACTGCCCTA  
TTGACAAGGGTTACATGCTGCTCACCTACTGCCCTGGGATTAATCAGTTACAGGCCAG  
AGTCTCCTGGAGGGCTGGAACTCTGAGTCCTCTATGAACCTCTGTAGCCTAAATGAAAT  
TCTAAAATACCGATGGAACAAAAAAAGGGCGGCCGACTCTAGAGTCG  
ACCTGCAGTAGGGATAACAGGGTAATAAGCTGGCCGCATGG

## FIGURE 153

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50911
><subunit 1 of 1, 348 aa, 1 stop
><MW: 39711, pI: 8.70, NX(S/T): 1
MAATLGPLGSWQQWRRCLSARDGSRMLLLLLLGSGQGPQQVGAGQTFEYLKREHSLSKPYQ
GVGTGSSSIWNLMGNAMVMTQYIRLTPDMQSKQGALWNRVPCFLRDWELQVHFKIHGQGKKN
LHGDSLAIWYTKDRMQPGPVFGNMDKFVGLGVFVDTYPNEEKQQERVFPYISAMVNNGSLSY
DHERDGRPTELGGCTAIVRNLYDTFLVIRYVKRHTIMMDIDGKHEWRDCIEVPGVRLPRG
YYFGTSSITGDLSDNHDVISLKLFELTVERTPEEEKLHRDVFLPSVDNMKLPEMTAPLPLS
GLALFLIVFFSLVFSVFAIVIGIILYNKWQEQRKRFY
```

**Signal sequence:**

amino acids 1-38

**Transmembrane domain:**

amino acids 310-329

## FIGURE 154

CCGAGCCGGCGCGCAGCGACGGAGCTGGGCCGCTGGACCATGGCGTGAGTGCAATCTACGGATCAGTCT  
CTGATGGTGGTCGTTAACCTCAGTGGGACTCAAGATTCCATGAAGAAAATCAGTTGCTTCATTCAAGAAT  
TGGGGTCTGGCTCAGAATTCCAGCTGGTAAAATCTTTCTAGAAAGAGGTTAATTATGCCTGCAGTCT  
GACATGTTCCCAGATTGAGGTAAAACATGAAGAGAAAATAGAATACTTAATAATGCTTTCCGCAACCGCTTCT  
TGCTGCTGCTGGCCCTGGCTGCGTGCTGGCCTTGTGAGCCTCAGGCTGCAGTCTCCACCTGATCCCAGGTGT  
CGACTCCTAAGAATGGAATGAGTAGCAAGAGTCGAAAGAGAATCATGCCCGACCCTGTGACGGAGCCCCCTGTGA  
CAGACCCCGTTATGAAGCTCTTTGACTGCAACATCCCCAGTGTGGCCGAGCGCAGCATGGAAGGTATGCC  
CGCATCATTAAAGCTGGCTCAGTGCATGTGTCATTGCCACGGAGACAGGTACCCACTGTATGTCAATTCCA  
AAACAAAGCAGCAGAAAATTGACTGCACTCTGGCTAACAGGAAACCGTATCACCCAAAATGGAAGCTTTCA  
TTAGTCACATGTCAAAAGGATCCGGAGCCTCTTCGAAAGCCCTTGAACTCCTGCCTCTTACCCAAATCACC  
CATTGTGAGATGGGAGAGCTCACACAGACAGGAGTTGTCAGCATTGCAAGAACGGTCAGCTGCTGAGGGATA  
TCTATCTAAAGAAACACAAACTCCTGCCAATGATTGGTCTGCAAGACCAGCTTATTTAGAGACCAGTGGAAAAA  
GCCGGACCCATAAAAGTGGGCTGGCCTTGCTTATGGCTTCTCCAGATTGACTGGAAGAAGATTATTCA  
GGCACCAAGTGCCTGTTCTGCTCTGGAAAGCTGCTATTGCCCGTAAGAAACCAAGTATCTGAAAAGGAGC  
AGCGTCGTCACTCCTACGTTGAAAACAGCCAGCTGGAGAAGACCTACGGGAGATGGCAAGATCGTGG  
ATGCCCCACCAAGCAGCTTAGAGCTGCCAACCCATAGACTCCATGCTCTGCCACTTCTGCCACAATGTCAGCT  
TTCCCTGTACCAAGAAATGGCTGTGTTGACATGGAGCACTCAAGGTAAATTAGACCCATCAGATCGAGGATGAAA  
GGGAAAGACGGGAGAAGAAAATTGACTTCGGTATTCTCCTGGGTGCCACCCCATCCTGAACCAAACCATCG  
GCCGGATGCACTGCCACCGAGGGCAGGAAAGAGCTTCTGGCCCTRACTCTGCTCATGATGTCACTCTGT  
CACCAAGTCTCAGTGCCTGGGCTTCAAGGCCAGGTTCCAAGGTTGCAAGGCCAGGTTGATCTTGAGCTT  
GGCAAGACAGAGAAAAGCCAGTGAACATTCCGCCGATTCTTACAATGGCGTCACTGTCACATTCCACACCT  
CTTCTGCCAAGACCAAGCCATTCTCCAAAGCCATGTGCCGCTTGAAAACATTGGCCGTTGTGAAA  
GGGACATGTTGAGCCCTGGGTGGCAGTGGTACAAATTATTATGATGCTAGTCACAGGGAAAGGATTCAAGG  
TATGCACTACAGCACTAGAATCCATGCCAATACAGAGCATAGGGAAAGGTCACATTCTAGTTGCTGTTAC  
TAAGGGTAGAAGATTATTGCTTTAAAGGCTAAATTATTGTTGTTGGAAACCACAGATGGTTGGGTTGAACAGT  
AAGCACATTGCTGCAATGTTGACGTGAATTGCTGGTACAAATGCCAGTTCAAGACCTGAAGTTGCCAATCCAAGTTGCAC  
TCTTCTGCCCTGCCCATGTTACTATGTGATGGAACCACAGCACACCTCAACCAAATTTTAATCTTAGACATT  
TTTACCTGTCCTGTTAAGAATTCTGTAAGTGAATTCTAAAGGTTGGCAAACCTTTCTGTAAG  
GCCAGATTGTAATATTCAGACTGTGGACCAAAAGGCCACATAACAGTCTCTGTCATAACTACTCAACTCTGT  
TTCTGAAGCAGGAAAGCCACCACAGACAGTACATAAAGGAATATGTGATGCTGGGTTCCAGGCCAGACAAAACA  
GATGGTGACCAACTTGGCCCTGGCTGTAGTTGCTGACCCCTCATCTAAAAAATAGGTATACTACAATTGC  
ACTTCCAGCACTTGAGAACGAGTTGAATACCAAGAATTATTCAATGGTTCCTCCAGTAACCTCTGCTAGAAACA  
CAGAATTGGCTGTATGACACTAGAACAAAATGAGGGTAAATAAACATTGAATTAGAATGAATCATAGAA  
AACTGATTAGAAGAATACCTGATGTTATGATGATTGTTAAGTATGTTCTAAATATTGTT  
CTGCTGAGTCATTTGCTGTATGCTGAAATTGTTGATGCCATTAGTATTGTTATAGTTAGGAAAATATT  
TTCTAAAGACCAAGTTAGATGACTCTTATTCTGCTAGTAATATTCAATTGCTGTCACCTGCTTGGTGGTTAGAAG  
GAGGCTAGAAGATGAATTCAAGGCACCTTCTCCAATAAAACTAATTATGGCTCATTCCTTGACAAGCTGTAGA  
ACTGGATTCTTTAAACCATTTCATCAGTTCAAAATGGTAAATTCTGATTGTTAAATGCGTTTTGGA  
AGAACTTTGCTATTAGGTAGTTACAGATCTTATAAGGTGTTATATATTAGAAGCAATTATAATTACATCTG  
TGATTCTGAACTAATGGTCTAATTAGAGAAATGGAAGTGAAAGTGAAGATTCTCTGTTGTCATCGGCATTCC  
AACTTTTCTCTTGTGTTGTCCAGTGTGCAATTGATGTTCTATAAATAAATTGTTAAGAATAA

## **FIGURE 155**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48329
><subunit 1 of 1, 480 aa, 1 stop
><MW: 55240, pI: 9.30, NX(S/T): 2
MLFRNRFLLLALAALLAFVSLSQLQFFHLIPVSTPKNGMSSKSRKRIMPDPVTEPPVTDPVY
EALLYCNIPSVAERSMEGHAPHFKLVSVHFIRHGDRYPLYVIPKTKRPEIDCTLVANRKP
YHPKLEAFISHMSKGSGASFESPLNSLPLYPNHLCEMGELTQTGVVQHLQNGQLLRDIYLK
KHKLPPNDWSADQLYLETTGKSRTLQSGLALLYGFLPDFDWKKIYFRHQPSALFCSCGSCYCP
VRNQYLEKEQRRQYLLRLKNSQLEKTYGEMAKIVDVPTKQLRAANPIDSMLCHFCHNVSFPC
TRNGCVDMEHFKVIKTHQIEDERERREKKLYFGYSLLGAHPILNQTIGRMQRATEGRKEELF
ALYSAHDVTLSPLSVLSEARFPRFAARLIFELWQDREKPSEHSVRLIYNGVDVTFHTSF
CQDHHKRSPKPMCPLENLVRFVKRDMFVALGGSGTNYYDACHREGF
```

**Signal sequence:**

amino acids 1-18

## **FIGURE 156**

AAAAAAGCTCACTAAAGTTCTATTAGAGCGAATACGGTAGATTCATCCCTTGAAGAACAGTACTGTGGA  
GCTATTTAAGAGATAAAAACGAAATATCCTTCTGGGAGTTCAAGATTGTGCAGTAATTGGTTAGGACTCTGAGC  
GCCGCTGTCACCAATCGGGAGAGAAAAGCGGAGATCCTGTCGCCCTGCACCGCCTGAAGCACAAAGCAGAT  
AGCTAGGAATGAACCATCCCTGGGAGTATGTGAAACAACGGAGGAGCTGTACTTCCAACGTCCCATTCTAT  
GGCGCAAGGAACGTCTGACTTCAGTGGTTAAGGGAGAATTGAAAATAATTCTGGAGGAAGATAAGAATGAT  
TCCCTGCGCAGCTGCACCGGGACTACAAAGGGCTGTCTGGGAATCCTCTGGGACTCTGTGGGAGACCGG  
ATGCACCCAGATAACGCTATTCACTTCCGGAAAGAGCTGGAGAAAGGCTCTAGGGTGGGAGCATCTCAGGGACCT  
GGGGCTGGAGCCCCGGGAGCTCGGGAGCGGGAGTCCGATCATCCCCAGAGGTAGGACGAGCTTTCGCCCT  
GAATCCCGCAGCGGAGCTGGTACGGCGGGAGGATAGACCGGGAGGAGCTGTATGGGGCCATCAAGTG  
TCAATTAAATCTAGACATTCTGATGGAGGATAAAAGTGAATTAGAAATAAAATTAGTGAATAGCAGCCACTGAGATGCGGTT  
CCCTCTACCCACGCCTGGATCCGGATATCGGAAGAACACTCTGAGAGCTACAGCCCAGACTCA  
CTTCTCCCTCATCGTCAAAATGGAGCCAGGGTAGTAAGTACCCGAATTGGTGTGAAACGCGCCCTGGACCG  
CGAAGAAAAGGCTGTCACCACTGGTCTTACGGCCTCGACGGGGCGACCCGGTGCACAGGCACCGCG  
CATCCGCGTGTGGTTCTGGATGCGAACGACAACGACCCAGCGTTGCTCAGCCCGAGTACCGCGCAGCGTTCC  
GGAGAATCTGGCCTTGGCACCGCAGCTGCTTGAGTCACAGCTACCGACCCCTGACGAAGGAGTCAATGCGGAAGT  
GAGGTATTCCCTCCGGTATGTGGACGACAAGGGCCCAAGTTTCAAACAGTATTGTAATTGGACAATATC  
AACAAATAGGGAGCTGGACCGAGGAGTCAGGATTCTACAGATGGAAGTGCAGAACGAAATGGATAATGAGGATA  
TTCTGCGCGAGCCAAAGTCCTGATCACTGTTCTGGACGTGAAACGACAATGCCCAGAGTGGTCTCACCTCTCT  
CGCCAGCTCGGTTCCCGAAAACTCTCCAGAGGGACATTAAATTGCCCTTTAAATGTAATGACCAAGATTCTGA  
GGAAAACGGACAGGTGATCTGTTCATCCAAAGGAATCTGCCCTTAAATTAGAAAAATCTTACGGAAATTACTA  
TAGTTTAGTCACAGACATAGCTGGATAGGAACAGGTTCTAGCTACACATCACAGTGACCGCCACTGACCG  
GGGAACCCGCCCTATCCACGAAACTCATCTCGCTGAACTGGCAGACACCAACGACAACCCGCCGGTCTT  
CCCTCAGGCCCTCTATCCGTTATATCCAGAGAACATCCAGAGGAGTTCCCTCGTCTGTGACCGCCCA  
CGACCCCGACTGTGAAGAGAACGCCCAGATCACTTATCCCTGGCTGAGAACACCATCCAAGGGCAAGCCTATC  
GTCCTACGTGTCATCAACTCCGACACTGGGTACTGTATGCGCTGAGCTCCTCGACTACGAGCAGTCCGAGA  
CTTGCAGTGAAGTGTGGCGGGACAACGGGACCCGCCCTCAGCAGAACGCTGTGAGCTGTCG  
GCTGGACCAGAACGACAATGCCCCGAGATCCTGTACCCGCCCTCCCACGGACGGTCCACTGGCGTGGAGCT  
GGCTCCCCGCTCCGAGAGCCGGTACCTGGTACCAAGGTGGTGGCGGTGGACAGAGACTCCGGCAGAACGC  
CTGGCTGCTTACCGTCTGCTCAAGGCCAGCGAGCCGGACTCTCTGGTGGGTCTGCACACGGCGAGGTGCG  
CACGGCGCAGGCCCTGCTGGACAGAGACGCGCTCAAGCAGAGCCTCGTAGTGGCGTCCAGGACCACGGCCAGC  
CCCTCTCTGCCACTGTACGCTACCGTGGCGTGGCGACAGCATCCCCAAGTCTGGCGGACTCGCAG  
CCTCGAGTCTCAGCTAACTCTGAAACCTCAGACCTCACTGTACCTGGTAGCGGTGGCCGGTCTCTG  
CGTCTTCCGTGCTCATCTGCTGCGCTCAGGCTGCGGCTGGACAAGTCAACGCTGTCAGGC  
TTCAAGGAGGGCTTGACAGGAGGCCGGCTCGCAGGGTGGACGGGGTGCAGGCTTCTGAGAC  
CTATTCCCACGAGGTTCCCTCACCACGGACTCGCGGAAGAGTCACCTGATCTTCCCAGCCAACTATGAGA  
CATGCTCGTCAGCCAGGAGAGCTTGAAGGGCCCTTTGCTGTCAAGGTGATTGGTATTCTAAAGA  
CAGTCATGGTTAATTGAGGTGAGTTATATCAAATCTCTTTCTTTTTTAATTGCTCTGTCTCCAAGC  
TGGAGTGCAGGGTACGATCATAGCTCACTGCGCCTCAAACCTTAGGCTCAAGCAATTATCCCACCTTGCT  
CCGGTGTAAACGGGACTCACGGTCAAGCCACCTACTGTCTGCCATCTATCTATCTATCTATCTAT  
CTATCTATCTATCTATCTATTACTTCTGTACAGACGGAGTCTCACGCCGTAACTCCAGTACTTGGGAGGC  
CGAGGGGGGGATCACGTGGAGGTTGGAGTTGAGACCCTGACCAACATGGAGAAACCCGTCTATAACTAA  
AAAAAATACAAAATTAGCCGGCGGGTGGAGGTGCAATGAGCTGAGATTGTGCCATTGCACTCCAGCTGGCAACAAGAGTG  
AAACTCTATCTCA

## **FIGURE 157**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48306
><subunit 1 of 1, 916 aa, 1 stop
><MW: 100204, pi: 4.92, NX(S/T): 4
MIPARLHRDYKGLVLLGILLGTLWETGCTQIRYSVPEELEKGSRVGDISRDLGLEPRELAER
GVRIIPRGRTQLFALNPRSGSLVTAGRIDREELCMGAIKCQLNLDILMEDKVKIYGVEVEVR
DINDNAPYFRESELEIKISENAATEMRFPPLPHAWDPDIGKNSLQSYLESPNTHFSLIVQNGA
DGSKYPELVLKRALDREEKAHHHLVLTASDGGDPVRTGTARIRVMVLDANDNAPAFFAQPEYR
ASVPENLALGTQLLVVNATDPDEGVNAEVRYSFYVDDKAAQVFKLCDNSGTISTIGELDHE
ESGFYQMEVQAMDNAGYSARAKVLITVLDVNDNAPEVVLTSASSVPENS PRGTLIALLNVN
DQDSEENGQVICFIQGNLPFKLEKSYGNYSLVTDIVLDREQVPSYNITVTATDRGTPPLST
ETHISLNVADTNNDNPVFPQASYSAYIPENNPRGVSLVSVAHDPCCEENAQITYSLAENTI
QGASLSSYVSINSDTGVLVALSSFDYEQFRDLQVKVMARDNGHPPLSNVSLSFVLDQNDN
APEILYPALPTDGSTGVELAPRSAEPGYLVTKVVAVDRDSGQNAWLSYRLLKASEPGLFSVG
LHTGEVRTARALLDRDALKQSLVVAVQDHGQPPLSATVTLTVAVADSIPQVLADLGSLESPA
NSETSDLTLYLVVAVAASCVFLAFVILLALRLRRWHKSRLLQASGGGLTGAPASHFVGVD
GVQAFLQTYSHESVSLTTDSRKSHLIFPQPNYADMVLVSQESFEKSEPLLSDSVFSKDSHGL
IEVSLYQIFFLFFFNCVSQAGVQRYDHSSLRPQTPRLKQLSHLCRRCNRDYRCKPPTVCLS
IYLSIYLSIYLSIYLLLSDGSLOTPVIPVLWEAEAGGSPEVGSLRPA
```

**Signal sequence:**

amino acids 1-30

**Transmembrane domains:**

amino acids 693-711, 809-823, 869-888

## FIGURE 158

CCCAGGCTCTAGTCAGGAGGAGAAGGAGGAGCAGGAGGTGGAGATTCCCAGTTAAAG  
GCTCCAGAACATCGTGTACCAGGCAGAGAACTGAAGTACTGGGGCCTCCTCCACTGGGTCCGAA  
TCAGTAGGTGACCCGCCCTGGATTCTGGAAGACCTCACCAATGGGACGCCCGACCTCGT  
GCGGCCAAGACGTGGATGTTCTGCTCTGCTGGGGGAGCCTGGCAGGACACTCCAGGGC  
ACAGGAGGACAAGGTGCTGGGGGTCACTGAGTGCCAACCCCATTGCAGCCTTGGCAGGC  
CCTTGTCCAGGGCCAGCAACTACTCTGTGGCGGTGTCTGTAGGTGGCAACTGGGTCTT  
ACAGCTGCCACTGTAAAAACCGAAATAACACAGTACGCCTGGAGACCACAGCCTACAGAA  
TAAAGATGGCCCAGAGCAAGAAATACCTGTGGTTCAGTCATCCCACACCCCTGCTACAACA  
GCAGCGATGTGGAGGACCACAACCATGATCTGATGCTTCAACTGCGTGACCAGGCATCC  
CTGGGGTCAAAGTGAAGCCATCAGCCTGGCAGATCATTGCACCCAGCCTGGCAGAAGTG  
CACCGTCTCAGGCTGGGCACTGTCACCAGTCCCCGAGAGAATTTCTGACACTCTCAACT  
GTGCAGAAGTAAAAATCTTCCCCAGAAGAAGTGTGAGGATGCTTACCCGGGCAGATCACA  
GATGGCATGGTCTGTGCAGGCAGCAGCAAAGGGCTGACACGTGCCAGGGCGATTCTGGAGG  
CCCCCTGGTGTGTGATGGTGCACTCCAGGGCATCACATCCTGGGCTCAGACCCCTGTGGGA  
GGTCCGACAAACCTGGCGTCTATACCAACATCTGCCGTACCTGGACTGGATCAAGAAGATC  
ATAGGCAGCAAGGGTGATTCTAGGATAAGCACTAGATCTCCCTTAATAAACTCACAACTCT  
CTGGTTC

## **FIGURE 159**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48336
<subunit 1 of 1, 260 aa, 1 stop
<MW: 28048, pI: 7.87, NX(S/T): 1
MGRPRPRAAKTWMFLLLGGAWAGHSRAQEDKVLGGHECOPHSQPWQAALFQGQQLLCGGVL
VGGNWVLTAAHCKKPKYTVRLGDHSLQNKGDPQEIPVVQSIPHPCYNSSDVEDHNHDLMLL
QLRDQASLGSKVVKPISSLADHCTQPGQKCTVSGWGTVTSPRENFPDTLNCAEVKIFPQKKCED
AYPGQITDGMVCAGSSKGADTCQGDGGPLVCDGALQGITSWGSDPCGRSDKPGVYTNICRY
LDWIKKIIGSKG
```

**Important Features:**

**Signal peptide:**

amino acids 1-23

**Transmembrane domain:**

amino acids 51-71

**N-glycosylation site.**

amino acids 110-113

**Serine proteases, trypsin family, histidine active site.**

amino acids 69-74 and 207-217

**Tyrosine kinase phosphorylation site.**

amino acids 182-188

**Kringle domain proteins motif**

amino acids 205-217

## FIGURE 160

GGCGCCGGTGCACCGGGCGGGCTGAGGCCTCTGCGGCCGGCTGCGGCCGGCG  
CGCGCCGCCAACGCCCCAACCCCGGCCGCCCCCTAGCCCCCGCCGGCCGCGCCCG  
GCCCGCGCCCAGGTGAGCGCTCCGCCCGCGAGGCCCGCCCCGGCCCGCCCCCG  
CCCCGGCCGGCGGGGAACCGGGCGGATTCTCGCGCTCAAACCACCTGATCCCATAAAAC  
ATTCATCCTCCCGGGCCCGCTGCGAGCGCCCGCCAGTCCGCGCCGCCGCCCCCTCG  
CCCTGTGCGCCCTGCGGCCCTGCGCACCCGCGGCCAGGCCAGGCCAGAGCCGGCGGAGC  
GGAGCGCGCCGAGCCTCGTCCCGCGGCCGGCCGGCCGTAGCGGCGGCCCTGGA  
TGCGGACCCGGCCGGGGAGACGGCGCCGCCGAAACGACTTCAGTCCCCGACGCGC  
CCCGCCAACCCCTACGTGAAGAGGGCGTCCGCTGGAGGGAGGCCGGCTGCTGGCATGGTG  
CTGTGGCTGCAGGCCTGGCAGGTGGCAGCCCCATGCCAGGTGCGTATGCTACAATGA  
GCCAAGGTGACGACAAGCTGCCCGAGCAGGGCTGCAGGCTGTGCCGTGGCATCCCTG  
CTGCCAGCCAGCGCATCTTCCTGCACGGCAACCGCATCTCGCATGTGCCAGCTGCCAGCTTC  
CGTGCCTGCCGCAACCTCACCATCCTGTGGCTGCACTCGAATGTGCTGGCCGAATTGATGC  
GGCTGCCTCACTGGCTGGCCACATTCCACGGCTGGGCCCTACACACGCTGCACCTGGACC  
GGTCTGTGGACCCCTGCCACATTCCACGGCTGGGCCCTACACACGCTGCACCTGGACC  
TGCGGCCTGCAGGAGCTGGGCCGGGCTGTTCCGCGGCCCTGGCTGCCCTGCAGTACCTCTA  
CCTGCAGGACAACCGCCTGCAGGCACTGCCTGATGACACCTCCGCGACCTGGCAACCTCA  
CACACCTCTCCTGCACGGCAACCGCATCTCAGCGTCCGGAGCGCGCTTCCGTGGGCTG  
CACAGCCTCGACCGTCTCCTACTGCACCAAGAACCGCTGGCCATGTGCACCCGATGCC  
CCGTGACCTTGGCCGCTCATGACACTCTATCTGTTGCCAACATCTATCAGCGCTGCC  
CTGAGGCCCTGGCCCCCTGCGTGCCTGCACTGAGGCTCAACGACAACCCCTGGGCTG  
TGTGACTGCCGGCACGCCACTCTGGGCTGGCTGCAAGTTCGCCGCTCTCC  
GGTGCCTGCAGCCTCCGCAACGCCCTGGCTGGCGTACCTCAAACGCCCTAGCTGCC  
ACCTGCAGGCTGCGCTGTGGCCACCGCCCTTACCATCCCCTGACCGGCAGGGCCACC  
GATGAGGAGCCGCTGGGCTTCCAAGTGCCTGCCAGCCAGATGCCGCTGACAAGGCC  
ACTGGAGCCTGGAAGACCAGCTTCCGGCAGGCAATGCCGTAAGGGACGCCGCTGCC  
ACAGCCCAGGGCAACGGCTCTGGCCACGGCACATCAATGACTCACCC  
CTGGCTCTGCTGAGCCCCCGCTACTGCAGTGCAGGCCGGAGGCTCCGAGCC  
CCCCACCTCGGCCCTGCCGGAGGCCAGGCTGTTCACGCAAGAACCGCACCC  
GCCGTCTGGCCAGGCAGGCCGGGTGGCGGACTGGTACTCAGAAGGCTCAGGTGCC  
CTACCCAGCCTCACCTGCAGCCTCACCCCCCTGGCCTGGCGCTGGTGTGGACAGTGC  
TGGGCCCTGCTTGACCCCAGCGACACAAGAGCGTGCAGCAGCCAGGTGTGTACATAC  
GGGGTCTCTCCACGCCGCAAGCCAGGCCGGCGGCCACCC  
GTCCCTCCCTGATGGACGCCGCTGCCGCCACCCCCATCTCCACCC  
TTCGGCGGCAGCGTTGTTCAAGAACGCCCTCCCACCC  
GCATTTATTTACTTGTAAAAATATCGGACGACGTGGAATAAGAGCTTTCTTAAA  
AAAA

## **FIGURE 161**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44184
><subunit 1 of 1, 473 aa, 1 stop
><MW: 50708, pI: 9.28, NX(S/T): 6
MKRASAGGSRLLAWVLWLQAWQVAAPCPGACVCYNEPKVTTSCPQQGLQAVPGIPAASQRI
FLHGNRISHVPAASFRCRNLTILWLHSNVLARIDAAFTGLALLEQLDLSDNAQLRSVDPA
TFHGLGRLHTLHLDRCGLQELGPGLFRGLAALQYLYLQDNALQALPDDTFRDLGNLTHLFLH
GNRISSVPERAFRGLHSLDRLLLHQNRVAHVPHAFRDLGRLMTLYLFANNLSALPTEALAP
LRALQYLRLNDNPWVCDCRARPLWAWLQKFRGSSSEVPCSLPQRLAGRDLKRLAANDLQGCA
VATGPYHPIWTGRATDEEPLGLPKCCQPDAADKASVLEPGRPASAGNALKGRVPPGDSPPGN
GSGPRHINDSPFGTLPGSAEPPLTAVRPEGSEPPGFPTSGPRRPGCSRKNRTRSHCRLGQA
GSGGGGTGDSEGSGALPSLTCSLTPLGLALVLWTVLGPC
```

**Important features:**

**Signal peptide:**

amino acids 1-26

**Leucine zipper pattern.**

amino acids 135-156

**Glycosaminoglycan attachment site.**

amino acids 436-439

**N-glycosylation site.**

amino acids 82-85, 179-183, 237-240, 372-375 and 423-426

**VWFC domain**

amino acids 411-425

## FIGURE 162

GGAAGTCCACGGGGAGCTTGGATGCCAAAGGGAGGACGGCTGGGTCTGGAGAGGACTAC  
TCACTGGCATATTCTGAGGTATCTGTAGAATAACCACAGCCTCAGATACTGGGACTTTAC  
AGTCCCACAGAACCGTCCTCCAGGAAGCTGAATCCAGCAAGAACAAATGGAGGCCAGCGGG  
AGCTCATTGCAGACAAAGGCAAGTCCTTTCTCCTTCTGGCTTATCTCTGGCG  
GGCGCGCGGGAACCTAGAAGCTATTCTGTGGTGGAGGAAACTGAGGGCAGCTCCTTGTAC  
CAATTAGCAAAGGACCTGGGTCTGGAGCAGAGGGAAATTCTCCAGGCGGGGGTAGGGTTG  
TTTCCAGAGGGAACAAACTACATTGCAGCTCAATCAGGAGACCCGGATTGTTGCTAAAT  
GAGAAATTGGACCGTGAGGATCTGTGGTACACAGAGCCCTGTGTGCTACGTTCCAAGT  
GTTGCTAGAGAGTCCTCGAGTTTCAAGCTGAGCTGCAAGTAATAGACATAAACGACC  
ACTCTCCAGTATTCTGGACAAACAATGTTGGTAAAGTATCAGAGAGCAGTCCTCCTGG  
ACTACGTTCTCTGAAGAATGCCGAAGACTTAGATGTAGGCCAAAACAATATTGAGAACTA  
TATAATCAGCCCCAACTCCTATTTCGGGTCTCACCAGCAACCGCAGTGTGATGGCAGGAAAT  
ACCCAGAGCTGGTGGTACAAAGCGCTGGACCGAGAGGAAGAAGCTGAGCTCAGGTTAAC  
CTCACAGCACTGGATGGTGGCTCTCCGCCAGATCTGCACTGCTCAGGCTACATCGAAGT  
CCTGGATGTCAACGATAATGCCCTGAATTGAGCAGCCTTCTATAGAGTGCAGATCTCTG  
AGGACAGTCCGGTAGGCTTCTGGTTGTGAAGGTCTGACACAGGATGTAGACACAGGAGTC  
AACGGAGAGATTCCTATTCACTTTCCAAGCTTCAGAAGAGATTGGAAAACCTTAAGAT  
CAATCCCTGACAGGAGAAATTGAACAAAAAAACAACTCGATTGAAACTTCAGTCCT  
ATGAAGTCAATATTGAGGCAAGAGATGCTGGAACCTTTCTGGAAAATGCACCGTCTGATT  
CAAGTGATAGATGTGAACGACCATGCCAGAAGTTACATGCTGCTTACAGATTTGATT  
ACCTGAGAACGCGCTGAAACTGTGGTGCACTTTCAGTGTTCAGATCTGATT  
AAAATGGAAAATTAGTTGCTCCATTCAAGGAGGATCTACCCCTCCTGAAATCCGCGGAA  
AACTTTACACCTACTAACGGAGAGACCACTAGACAGAGAACGAGACGGGAATACAACAT  
CACTATCACTGTCACTGACTTGGGACCCCTATGCTGATAACACAGCTCAATATGACCGTGC  
TGATGCCGATGTCAATGACAACGCTCCGCCCTCACCCAAACCTCCTACACCCCTGTC  
CGCGAGAACACAGCCCCGCCCTGCACATCCGCACTCGCTCAGCGCTACAGACAGAGACTCAGG  
CACCAACGCCAGGTACCTACTCGCTGCTGCCAGGACCCGACCTGCCCTCACAT  
CCCTGGTCTCCATCAACGCCAACACGGCCACCTGTTGCCCTCAGGTCTCTGGACTACGAG  
GCCCTGCAGGGTTCCAGTCCGCGTGGCGCTTCAGACCGACGGCTCCCGCGCTGAGCAG  
CGAGGCGCTGGTGCCTGGTGGCTGGACGCCAACGACAACCTGCCCTCGTGTGTAC  
CGCTGCAGAACGGCTCCGCCCTGCACCGAGCTGGTCCCCGGCGGCGAGCCGGCTAC  
CTGGTGACCAAGGTGGTGGCGTGGACGGCACTCGGCCAGAACGCTGGCTGTC  
GCTGCTCAAGGCCACGGAGCTCGGTCTGTTGGCGTGTGGCGACAATGGCGAGGTGCGCA  
CCGCCAGGCTGCTGAGCGAGCGCAACGCCAACGACAACCTGCCCTCGTGTGTAC  
AATGGCGAGCCTCCGCGCTGGCCACCGCACGCTGCACGTGCTCCTGGTGACGGCTTC  
CCAGCCCTACCTGCCCTCCGGAGGGCGCCACCCAGGCCAGGCCACTGCTCACCG  
TCTACCTGGTGGTGGCGTGGCTCGGTCTTCGCTTCCCTTTGGTGCTCCTGTT  
GTGGCGGTGCCTGGCTGTAGGAGGAGCAGGGCGGCCCTGGTGGTGCTGCTTGGTGCCGA  
GGGCCCTCCAGGGCATCTTGTGGACATGAGCGGCCAGGCCACTCCAGAGCTACC  
AGTATGAGGTGTCTGGCAGGAGGCTCAGGGACCAATGAGTTCAAGTCTGAAGCCGATT  
ATCCCCAACCTCCCTCCCAGTGCCCTGGAAAGAAATACAAGGAAATTCTACCTCCCCAA  
TAACCTTGGTCAATATTCAGTGAACATAGTGAATTACATTCCATAGGTATT  
TGTGGCATTTCCATGCCAATGTTATTCCCCAATTGTGTATGAAATTGACGGAT  
TTACTCTGATTTCTCATGTTCTCCCTTGTAAAGTGAACATTACCTTATT  
CCTGGTTCTT

## FIGURE 163

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48314
<subunit 1 of 1, 798 aa, 1 stop
<MW: 87552, pI: 4.84, NX(S/T): 5
MEASGKLICRQRQVLFSLLLGLSLAGAAEPRSYSVVEETEGSSFVTNLAKDLGLEQREFSR
RGVRVVSRGNKLHLQLNQETADLLLNEKLDREDLCGHTEPVCVLRFQVLLESPFEFFQAELOV
IDINDHSPVFLDKQMLVKVSESSPPGTTFPLKNAEDLDVGQNNIENYIISPNSYFRVLTRKR
SDGRKYPELVLKDALKALDREEEAELRLTLTALDGGSPPRSGTAQVYIEVLDVNDNAPEFEQPFY
RVQISEDSPVGFLVVKVSATDVDTGVNGEISYSLFQASEEIGKTFKINPLTGEIELKKQLDF
EKLQSDEVNIEARDAGTFSGKCTVLIQVIDVNDHAPEVTMSAFTSPIPENAPETVVALFSVS
DLDSENGKISCSIQEDLPFLLKSAENFYTLTERPLDRESRAEYNITITVTDLGTPMILITQ
LNMTVLIADVNDNAPAFQTSYTLFVRENNSPALHIRSVSATDRDGTNAQVTYSLLPPQDP
HLPLTSLVSINADNGHLFALRSLDYEALQGFQFRVGASDHGSPALSSEALVRVVVLDANDNS
PFVLYPLQNGSAPCTELVPRAAEPGYLVTKVAVDGDSGQNAWLSYQLLKATELGLFGVWAH
NGEVRTARLLSERDAAKHRLVVLVKDNNGEPPRSATATLHVLLVDGFSQPYLPLPEAAPTQAQ
ADLLTVYLVVALASVSSLFLFSVLLFVAVRLCRRSRAASVGRCLVPEGPLPGHLVDMMSGRT
LSQSYQYEVCLAGGSGTNEFKFLKPIIPNFPPQCPGKEIQGNSTFPNNFGFNIQ
```

**Important features:**

**Signal peptide:**

amino acids 1-26

**Transmembrane domain:**

amino acids 685-712

**Cadherins extracellular repeated domain signature.**

amino acids 122-132, 231-241, 336-346, 439-449 and 549-559

**ATP/GTP-binding site motif A (P-loop).**

amino acids 285-292

**N-glycosylation site.**

amino acids 418-421, 436-439, 567-570 and 786-789

## **FIGURE 164**

ACCCACGCGTCCGCCACGCGTCCGCCACGCGTCCGCCACGCGTCCGCCGTAGCGTGC  
GCCGATTGCCTCTGGCCTGGCAATGGTCCGGCTGCCGGTCACGACCGCCCCCGCGTCAT  
GCGGCTCCTCGGCTGGTGGCAAGTATTGCTGTGGTGCTGGACTTCCGTCACCGCGTGG  
AGGTTGCAGAGGAAAGTGGTCGTTATGGTCAGAGGAGCAGCCTGCTCACCTCTCAGGTG  
GGGGCTGTGTACCTGGGTGAGGAGGAGCTCCTGCATGACCCGATGGCCAGGACAGGGCAGC  
AGAAGAGGCCAATGCGGTGCTGGGCTGGACACCCAAGGCGATCACATGGTGTGCTG  
TGATTCCCTGGGAAGCTGAGGACAAAGTGAGTCAGAGCCTAGCGCGTCACCTGTGGTGT  
GGAGGAGCGGAGGACTCAAGGTGCAACGTCCGAGAGAGCCTTCTCTGGATGGCGCTGG  
AGCACACTCCCTGACAGAGAACAGGAGTATTACACAGAGCCAGAAGTGGCGGAATCTGACG  
CAGCCCCGACAGAGGACTCCAATAACACTGAAAGTCTGAAATCCCCAAGGTGAACGTGAG  
GAGAGAACATTACAGGATTAGAAAATTCACTCTGAAAATTAAATATGTCACAGGACCT  
TATGGATTTCTGAACCCAAACGGTAGTGACTGTACTCTAGCCTGTTACACCCGTGGT  
GCCGCTTCTGCCAGTTGGCCCTCACTTAACCTCTGCCCCGGCATTCCAGCTCTT  
CACTTTTGGCACTGGATGCATCTCAGCACAGCAGCCTTCTACCAGGTTGGCACCGTAGC  
TGTCCTAATATTTATTATTCAAGGAGCTAACCAATGCCAGATTAAATCATACAGATC  
GAACACTGGAAACACTGAAAATCTCATTAAATCAGACAGGTATAGAACCAAGAAGAAT  
GTGGTGGTAACTCAAGCGACCAAATAGGCCCTTCCAGCAGCTTGATAAAAAGTGTGGA  
CTGGTTGCTGTATTTCTTATTCTTTAATTAGTTTATTATGTATGCTACCATTGAA  
CTGAGAGTATTGGGGCTAATTCCAGGACAAGAGCAGGAACATGTGGAGTAGTGATGGTCT  
GAAAGAAGTGGAAAGAGGAACCTCAATCCTCGTTAGAAATTAGTGCTACAGTTCTATA  
CATTCTCCAGTGACGTGTTGACTTGAAACTCAGGCAGATTAAAAGAACATTGTTGAA  
CAACTGAATGTATAAAAAAATTATAAACTGGTGTAACTAGTATTGCAATAAGCAAATGC  
AAAAATATTCAATAG

## **FIGURE 165**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48333
><subunit 1 of 1, 360 aa, 1 stop
><MW: 39885, pI: 4.79, NX(S/T): 7
MVPAAGRRPPRVMRLLGWWQVLLWVLGLPVRGVEVAEESGRLWSEEQPAHPLQVGAVYLGE
ELLHDPMGQDRAEEANAVLGLDTQGDHMVMLSVPGEAEDKVSSEPSGVTCGAGGAEDSRC
NVRESLFSLDGAGAHFPDREEEYYTEPEVAESDAAPTEDSNNTESLKSPKVNCERNITGLE
NFTLKILNMSQDLMDFLNPNGSDCTLVLFYTPWCRFSASLAPHFNSLPRAFFPALHFLALDAS
QHSSLSTRFGTVAVPNILLFQGAKPMARFNHTDRTLETLKIFIFNQTGIEAKKNVVVTQADQ
IGPLPSTLIKSVDWLLVFSLFFLISFIMYATIRTESIRWLIPGQEQEHV
```

**Important features:**

**Signal peptide:**

amino acids 1-25

**Transmembrane domain:**

amino acids 321-340

**Homologous region to dilsufide isomerase**

amino acids 212-302

**N-glycosylation site.**

amino acids 165-168, 181-184, 187-190, 194-197, 206-209, 278-281  
and 293-296

**Thioredoxin domain**

amino acids 211-227

## **FIGURE 166**

CCCGGCTCCGCTCCCTCTGCCCTCGGGTCGCGGCCACGATGCTGCAGGCCCTGGCT  
CGCTGCTGCTGCTCTCCTCGCCTCGCACTGCTGCCTGGCTCGCGCGGGCTTCCCTC  
TTTGGCCAGCCGACTTCTCCTACAAGCGCAGCAATTGCAAGCCCACCGTCAACCTGCA  
GCTGTGCCACGGCATCGAATACCAGAACATGCGGCTGCCAACCTGCTGGCCACGAGACCA  
TGAAGGAGGTGCTGGAGCAGGCCGGCTTGGATCCCGCTGGTCATGAAGCAGTGCCACCCG  
GACACCAAGAAGTTCCTGTGCTCGCTTCGCCCGTCTGCCTCGATGACCTAGACGAGAC  
CATCCAGCCATGCCACTCGCTCTGCGTGCAGGTGAAGGACCGCTGCCCGGTATGTCCG  
CCTTCGGCTTCCCGACATGCTTGAGTGCACCGTTCCCCCAGGACAACGACCTT  
TGCATCCCCCTCGCTAGCAGCACCTCCTGCCAGCCACCGAGGAAGCTCAAAGGTATG  
TGAAGCCTGCAAAATAAAATGATGATGACAACGACATAATGAAACGCTTGAAATG  
ATTTGCACTGAAAATAAAAGTGAAGGAGATAACCTACATCAACCGAGATACCAAAATCATC  
CTGGAGACCAAGAGCAAGACCATTACAAGCTGAACGGTGTCCGAAAGGGACCTGAAGAA  
ATCGGTGCTGTGGCTCAAAGACAGCTTGCAGTGCACCTGTGAGGAGATGAACGACATCAACG  
CGCCCTATCTGGTCATGGACAGAAACAGGGGGAGCTGGTATCACCTCGGTGAAGCGG  
TGGCAGAAGGGCAGAGAGAGTTCAAGCGATCTCCCGCAGCATCCGCAAGCTGCAGTGCTA  
GTCCCGGCATCCTGATGGCTCCGACAGGCCTGCTCCAGAGCACGGCTGACCATTCTGCTCC  
GGGATCTCAGCTCCGTTCCCAAGCACACTCCTAGCTGCTCCAGTCTCAGCCTGGCAGCT  
TCCCCCTGCCTTTGCACGTTGCATCCCCAGCATTCTGAGTTATAAGGCCACAGGAGTG  
GATAGCTGTTTACCTAAAGGAAAAGCCCACCCGAATCTGTAGAAATATTCAAACTAATA  
AAATCATGAATATTTAA

## **FIGURE 167**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50920
><subunit 1 of 1, 295 aa, 1 stop
><MW: 33518, pI: 7.74, NX(S/T): 0
MLQGPGSLLLLFLASHCCLGSARGLFLFGQPDFSYKRSNCKPIPVNQLCHGIEYQNMRLPN
LLGHETMKEVLEQAGAWIPLVMKQCHPDTKKFLCSLFAPVCLDDLDETIQPCHSLCVQVKDR
CAPVMSAFGFPWPDMLECDRFPQDNDLCIPLASSDHLLPATEEAPKVCEACKKNDDNDIM
ETLCKNDFALKIKVKEITYINRDTKIILETKSktiyKLNGVSERDLKKSVLWLKDSDLQCTCE
EMNDINAPYLVMGQKQGGELVITSVKRWQKGQREFKRISRSIRKLQC
```

**Important features:**

**Signal peptide:**

amino acids 1-20

**Cysteine rich domain, homologous to frizzled N terminus**

amino acids 6-153

## **FIGURE 168**

GTGGAGGCCGCGACGATGGCGGGCCGACGGAGGCCGAGACGGGGTTGGCGAGCCCCGGG  
CCCTGTGCGCGCAGCGGGCCACCGCACCTACGCGCCGCTGGTGTTCCTGCTCGCATC  
AGCCTGCTCAACTGCTCCAAGCCACGCTGTGGCTCAGCTTGACCTGTGGCTACGTCAT  
TGCTGAGGACTTGGTCCTGTCCATGGAGCAGATCAACTGGCTGTCACTGGTCTACCTCGTGG  
TATCCACCCCATTGGCGTGGCGGCATCTGGATCCTGGACTCCGTGGCTCCGTGGCG  
ACCATCCTGGGTGGCTGAACTTGCCCTCATGGGTGGCCAGAGCCTGTGCCCTGCATGGT  
TGTGGGACCCAAACCCATTGCCCTCATGGGTGGCCAGAGCCTGTGCCCTGCATGGC  
AGAGCCTGGTCATCTTCTCTCCAGCCAAGCTGGCTGCCCTGTGGTCCCAGAGCACCAGCGA  
GCCACGGCCAACATGCTGCCACCATGTCGAACCCCTGGCGTCCCTGTGGCAATGTGCT  
GTCCCCTGTGCTGGTCAAGAAGGGTGAGGACATTCCGTTAATGCTCGGTGTCTATACCATCC  
CTGCTGGCGTCGTCTGCCCTGTCCACCATGTCCTGTGGAGAGTGTGCCCTGGCG  
CCCTCTGCCGGGCTGCCAGCTCCACCTCAGAGAAGTCCTGGATGGCTCAAGCTGCAGCT  
CATGTGGAACAAGGCCTATGTCATCCTGGCTGTGCTTGGGGAAATGATCGGATCTCTG  
CCAGCTTCTCAGCCCTCCTGGAGCAGATCCTGTGCAAGCGGCCACTCCAGTGGGTTTCC  
GGCCTCTGTGGCGCTCTTCATCACGTTGGATCCTGGGGCACTGGCTCTGGCCCTA  
TGTGGACGGACCAAGCACTCACTGAGGCCACCAAGATTGGCCTGTGCCCTCTCTGG  
CCTGCGTGCCCTTGGCTGGCTCCAGCTGCAGGGACAGACCCCTGGCCCTGGCTGCCACC  
TGCTCGCTGCTGGCTGTTGGCTCTCGGTGGGCCCTGGCCATGGAGTTGGCGGTGCA  
GTGTTCTCCCCGTGGGGAGGGGGCTGCCACAGGCATGATTTGTGCTGGGAGGCC  
AGGGAAATACTCATGCTGGCAATGACGGCACTGACTGTGCGACGCTGGAGGCCCTTG  
TCCACCTGCCAGCAGGGGAGGATCCACTTGACTGGACAGTGTCTCTGCTGATGGCGG  
CCTGTGCACCTTCTCAGCTGCATCCTGGCGTCTTCCACACCCATACGGCGCCTGC  
AGGCCGAGTCTGGGGAGCCCCCTCCACCCGTAACGCCGTGGCGCGCAGACTCAGGGCG  
GGTGTGGACCGAGGGGAGCAGGAAGGGCTGGGTCTGGGCCAGCACGGCACTCCGGA  
GTGCACGGCGAGGGGGCTCGTAGAGGACCCAGAGGGCCGGAGCCCCACCCAGCCT  
GCCACCGAGCGACTCCCCGTGCGCAAGGCCAGCAGCCACCGACGCGCCCTCCGCC  
AGACTCGCAGGCAGGGTCCAAGCGTCCAGGTTATTGACCCGGCTGGTCTCACTCCT  
CTCCTCCCCGTGGTGATCACGTAGCTGAGCGCCTGTAGTCCAGGTTGCCGCCACATCGA  
TGGAGGCGAACTGGAACATCTGGTCACCTGCGGGCGGGGGCAAAGGGCTCCTGCGGGCT  
CCGGGAGCGAATTACAAGCGCGCACCTGAAAA

## **FIGURE 169**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50988
><subunit 1 of 1, 560 aa, 1 stop
><MW: 58427, pI: 6.86, NX(S/T): 2
MAGPTEAETGLAEPRALCAQRGHRTYARRWFLLAISLLNCSNATLWLSFAPVADVIAEDLV
LSMEQINWLSLVLYVSTPFGVAAIWILDVGRLRAATILGAWLNFAGSVLRMVPCMVGQTQN
PFAFLMGGQSLCALAQSLVIFSPAKLAALWFPEHQRATANMLATMSNPLGVLVANVLSPVLV
KKGEDIPLMLGVYTIPAGVVCLLSTICLWESVPPTPPSAGAASSTSEKFLDGLKLQLMWNK
YVILAVCLGGMIGISASFSALEQILCASGHSSGFSGLCALFITFGILGALALGPYVDRTK
HFTEAUTKIGLCLFSLACVPFALVSQQLQGQTLALAATCSLLGLFGFSVGPVAMELAVECSFPV
GEGAATGMI FVLGQAEGILIMLAMTALTIVRSEPSLSTCQQGEDPLDWTVSLLL MAGLCTFF
SCILAVFFHTPYRRLQAESGEPPSTRNAVGGADSGPGVDRGGAGRAGVLGPSTATPECTARG
ASLEDPRGPGSPHPACHRATPRAQPAATDAPS RPGRLAGRVQASRFIDPAGSHSSFSSPWVIT
```

**Important features:**

**Signal peptide:**

amino acids 1-44

**Transmembrane domains:**

amino acids 61-79, 98-112, 126-146, 169-182, 201-215, 248-268,  
280-300, 318-337, 341-357, 375-387, 420-441

**N-glycosylation site.**

amino acids 40-43 and 43-46

**Glycosaminoglycan attachment site.**

amino acids 468-471

## **FIGURE 170**

GTCCCACATCTGCTCAACTGGGTCAAGGTCCCTCTAGACCAGCTTGTCATCATTTGCTGAAGTGGACCAAC  
TAGTTCCCAGTAGGGGTCTCCCTGGCAATTCTGATCGCGTTGGACATCTCAGATCGCTTCCAATGAAGA  
TGGCCTTGCCTGGGTCTGTTCAATACTCATCTAACTATGGGACAAGGTTGTGCCGGCAGCTGGGG  
AAGAGCACGGGCTGATCAAGCCATCCAGGAAACACTGGAGGACTGTCCAGGCTTGAAGAAACTCTAGTGGT  
TCTGAATCTAGCCCCTGGCGGTAGCAGTGAATTGCAACTCTGCAACTTCTGCTGGGCTTTGGGCAGGGTGG  
CTACTTATTCCTTGTAGGGATTGTCAAGGAGGTGACCACTCTCACGGTGAATAACCAAGTGTCAAGAGGAAGTGCC  
ATCTGGTACAGTGATCGGGAAAGCTGTCCCAGGAACACTGGGGGGAGGAGAGGCGAGGCAAGCTGGGGCCGCTT  
CCAGGTGTTGAGCTGCCAGGCGCTCCCCATTAGGTGACTCTGAGGAAGGCTTGTCAACCACAGGCAGGG  
GCTGGATCGAGAGCAGCTGCGCAGACTGGGATCCCTGGCTGGTTCTTGATGTGCTTGCCACAGGGGATT  
GGCTCTGATCCATGTGGAGATCCAAGTGTGGACATCAATGACCACAGCCACGGTTCCCAAAGGCAGCAGGA  
GCTGGAAATCTCTGAGAGCGCTCTGCAACCCGGATCCCCCTGGACAGAGCTTGTACCCAGACACAGGCC  
TAACACCCTGCACACCTACACTCTGCTCCAGTGAACCTTGCCCTGGATGTCAATTGTGGCCCTGATGAGAC  
CAAACATGCAGAACTCATAGTGGTGAAGGAGCTGGACAGGAAATCATTCACTTTTGATCTGGTGTAACTGC  
CTATGACAATGGGAAACCCCCCAAGTCAGGTACCAAGCTGGAAATCCAAGAAGATGCTGCACCTGGTACCTCTCATAAAACT  
CCCTGCGTTGCTGAGAGTTCACTGGCACTGGAAATCCAAGAAGATGCTGCACCTGGTACCTCTCATAAAACT  
GACCGCCACAGACCCCTGACCAAGGCCCAATGGGAGGTTGAGTCTTCTCAGTAAGCACATGCCTCAGAGGT  
GCTGGCACCTCAGTATTGATGCCAACAGACAGGCCAGGTCTTCTGCGTCACCTCTAGACTATGAAAAGAACCC  
TGCCTACGAGGTGGATGTTCAAGGCAAGGGACCTGGGCTTCAATCCTATCCCAGGCCATTGCAAAGTTCTCATCAA  
GGTCTGGATGTCATAACATCCCAAGCATCCACGTACATGGGCTCCAGCCATCTGGTGTCAAGC  
TCTTCCAAGGACAGTTTATTGCTCTGTCATGGCAGATGACTTGAGATTCAAGGACACAATGGTTTGGTCCACTG  
CTGGCTGAGCCAAGAGCTGGGCAACTCAGGCTGAAAAGAACTAATGGCAACACATACATGTTGCTAACCAATGC  
CACACTGGACAGAGGAGCAGTGGCCAAATATACCCACTCTGTTAGCCAAGGACCAAGGACTCCAGGCCCTATC  
AGCCAAGAAACAGCTCAGCATTCAAGATCAGTGAACATCAACGACAATGCACCTGTGTTGAGAAAAGCAGGTATGA  
AGTCTCACGGGGAAACAAACTTACCCCTCTTCACTTCAAGGCTCATGATGCAAGACTGGCAT  
TAATGGAAAAGTCTCATACCGCATCAGGACTCCCAGTGTCTCAATTAGCTATTGACTCCAACACAGGAGA  
GGTCACTGTCAGAGGTCACTGAACATGAAGAGATGGCGGCTTGAGTTCCAGGTGATCGCAGAGGACAGCGG  
GCAACCCATGCTGCACTCAGTGTCTGTGGTCAAGCTCTGGATGCCATGATAATGCCAGGGTGGT  
CCAGCCTGTGTCAGCGATGGAAAGCCAGCCTCTCCGTGCTTGTGAATGCCCAACAGGCCACCTGCTGGTGCC  
CATCGAGACTCCAAATGGCTGGGCCAGCGGGACTGACACACCTCACTGGCACTCACAGCTCCGGCATT  
CCTTGACAACCATTGTCAGAGGATGCAAGACTCGGGGCAAATGGAGAGGCCCTACAGCATCGCAATGG  
AAATGAAGCCCACCTCTCATCCTCAACCCCTACAGGGCAGCTGGTCAATGTCACCAATGCCAGCAGCCT  
CATTGGAGTGAGTGGAGCTGGAGATAGTAGAGGACCAAGGGAAAGCCCCCTTACAGACCCGAGCCCTGTT  
GAGGGTCATGTTGTCAACAGTGTGACCCACTGAGGGACTCAGGCCAGCCTGGGCCCTGAGCATGTCGAT  
GCTGACGGTGTCTGGCTGTACTGTTGGCATCTGGGTTGATCTGGCTTGTTCATGTCATCTGCCG  
GACAGAAAAGGACAAACAGGCCATCAACTGTCGGAGGGCCAGTCCACCTACGCCAGCAGGCCAAGAGGCC  
CCAGAAACACATTCAAGAGGCAAGACATCCACCTCGTGCCTGTCAAGGGTCAAGGCTGGGAGCCTGTCAGGCC  
CGGGCAGTCCCACAAAGATGTTGACAGGGAGCTGGATGAGGAAAGCAGGCTGGGAGCCCTGCTGCAAGGCC  
CCACCTACCCGACCCCTGACAGGAGCTGCCGTAATCAAGCAACAGGGAGCACCGGGAGAGGCCAGAGG  
GCTGCAAGACACGGTCAACCTCTTCAACCATCCAGGCAAGGAAATGCCCTCCGGAGAACCTGAACCTTC  
CGAGCCCCAGCCTGCCACAGGCCAGCCAGTCCAGGCTCTGCAAGGTTGCAAGGCCACAGGGAGGCTGGC  
TGGAGACCAAGGGCAGTGAGGAAGCCCCACAGAGGCCACAGGCTCTGCAACCCCTGAGACGGCAGGACATCT  
CAATGGCAAAGTGTCCCCGTAGAAAATCAGGGCCCCGTCAAGATCCTGCGGAGCCTGGCTGTC  
TGCCCTCGCCAGCGGAACCCCGTGGAGGAGCTCACTGTTGATTCTCTCTGTCAGCAAATCTCCAGCTGCT  
GTCTTGCTGTCATCAGGGCAATTCCAGCCAAACCAACCGAGGAAATAAGTACTTGGCCAAGGCCAGGAGG  
CAGCAGGAGTCAATCCCAGACACAGATGGCCAAGTGAAGGGCTGGAGGCCAGACAGACCCAGAACAGGAGG  
AGGGCCTTGGATCCTGAAGAGGACCTCTGTGAAGCAACTGCTAGAAGAAGAGCTGTCAAGTCTGCTGGACCC  
CAGCACAGGTCTGGCCCTGGACCGGCTGAGCGCCCTGACCCGGCTGGATGGCGAGACTCTCTTGCCCTCAC  
CACCAACTACCGTGACAATGTGATCTCCCGGATGTCAGCCACGGAGGAGGCCAGCTCCAGACGTTCGG  
CAAGGCAGAGGCCACAGAGCTGAGCCAACAGGCACGGCTGGCCAGCACCTTGTCTGGAGATGAGCTCACT  
GCTGGAGATGCTGCTGGACAGCGCTCCAGCATGCCCTGGAGGCCCTGGAGGCCAGCTGCG  
CTGGGGAGGACCCCTGAGTTAGACTTGGCACCCAGTGCAAGGCTCAGGCATGAAAGTGAAGGGACCCAGGTGG  
AAAGACGGGAACTGAGGGCAAGAGCAGAGGCAGCAGCAGCAGCAGCAGGCTGTGAAACATACTCAGACGCC  
CTGGATCCAAGAACCCAGGGGCTGAGGATCTGTTGACAAGAGGCTGGTTCTAAATCTTGTAACTCACTAGCTAG  
CGGGGGCTGAGAACCTTGGGTGACTGATGCTACCCCCAACAGAGGAGGCAAGAGGCCAGGACTAACAGCTGAC  
TGACCAAAGCAGCCCCCTGTAAGCAGTCTGAGCTTGGAGGACAGGGACGGGCTGGAGATAAGTGT  
TCCTGGCAAAACATATGTTGAGCAGGACAAAGGGTCAAGTCTGGCAGAACAGATGCCACGGAGTATCACAGGCAGG  
AAAGGGTGGCCTTCTGGGTAGCAGGAGTCAGGGGCTGTACCCCTGGGGTGCCAGGAATGCTCTGACCTAT  
CAATAAGGAAAAGCAGTAAAAAAAAAAAAAA

## FIGURE 171

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48331
<subunit 1 of 1, 1184 aa, 1 stop
<MW: 129022, pI: 5.20, NX(S/T): 5
MMQLLQLLLGPGGYLFLLGDCQEVTTLTVKYQVSEEVPSGTIVGKLSQELGREERRQA
GAAFQVLQLPQALPIQVDSEEGLSTGRRLDREQLCRQWDPCLVSDVLATGDLALIHVEIQ
VLDINDHQPRFPKGQELEISESASLRTRIPLDRALDPDTGPNTLHTYTLSPSEHFALDVIV
GPDETKHAELIVVKELDREIHSFFDLVLTAYDNGNPPKGTSLVKVNVLDNSNDNSPAFAESS
LALEIQEDAAPGTLLIKLTATDPDQGPNGEVEFFLSKHMPPEVLDTFSIDAKTGQVILRRPL
DYEKNPAYEVDVQARDLGPNPIPAHCKVLIKVLVDVNDNIPSIHVTWASQPSLVSEALPKDSF
IALVMADDLDSGHNGLVCWLSQELGHFRLKRTNGNTYMLLTNATLDREQWPKYTLTLLAQD
QGLQPLSAKKQLSIQISDINDNAPVFEKSRYEVSTRENNLPSLHLITIKAHADLGIN GKVS
YRIQDSPVAHLVAIDSNTGEVTAQRSINYEMAGFEFQVIAEDSGQPMIASSSVWVVSLLDA
NDNAPEVVQPVLSDGKASLSVLVNASTGHLLVPIETPNGLGPAGTDTPPLATHSSRPFLTT
IVARDADSGANGEPLYSIRNGNEAHLFILNPHTGQLFVNVTNASSLIGSEWELEIVVEDQGS
PPLQTRALLRVMFVTSDHLDARSARKPGALSMSMLTVICLAVLLGIFGLLIALFMSICRTEK
KDNRAYNCREAESTYRQQPKRPQKHIQKADIHLVPVLRGQAGEPCEVGQSHKDVDKEAMMEA
GWDPCLQAFHLPHTLYRTLRNQGNQGAPAESREVLQDTVNLLFNHPRQRNASRENNLPEP
QPATGQPRS RPLKVAGSPTGRLAGDQGSEEAPQRPPASSATLRRQRHLNGKVSPEKE SGPRQ
ILRSLVRLSVAFAERNPVEELTVDSPPVQQISQLLSSLLHQGQFQPKPNHRGNKYLAKPGGS
RSAIPDTDGPSARAGGQTDPEQEEGPLDPEE DLSVKQLLEEELSSLDPSTGLALDRLSAPD
PAWMARLSSLPLTTNYRDNVISPDAAAATEEPRTFQTFGKAEAPELSPTGTRLASTFVSEMSSL
LEM LLEQRSSMPVEAASEALRRLSVCGRTLSLDLATSAASGMKVQGDPGGKTGTEGKSRGSS
SSSRCL
```

**Important features:**

**Signal peptide:**

amino acids 1-13

**Transmembrane domain:**

amino acids 719-739

**N-glycosylation site.**

amino acids 415-418, 582-585, 659-662, 662-665 and 857-860

**Cadherins extracellular repeated domain signature.**

amino acids 123-133, 232-242, 340-350, 448-458 and 553-563

## **FIGURE 172**

CGGACGCGTGGCGGACGCGTGGGGAGAGCCGAGTCCGGCTGCAGCACCTGGAGAAGG  
CAGACCGTGTGAGGGGGCCTGTGGCCCCAGCGTGCTGTGGCTCGGGAGTGGAAAGTGGAG  
GCAGGAGCCTCCTAACACTCGCCATGAGTTCCTCATCGACTCCAGCATCATGATTACCT  
CCCAGATACTATTTTGATTGGCTTCTTCATGCGCCAATTGTTAAAGACTAT  
GAGATACTGAGTACAGGTGATCTCTCCGTGACGTTGCATTTCATGGCACCCT  
GTTGAGCTCATCATCTTGAAATCTTAGGAGTATTGAATAGCAGCTCCGTTATTTC  
GGAAAATGAACCTGTGTGAATTCTGCTGATCCTGGTTTCATGGTGCCTTTACATTGGC  
TATTTATTGTGAGCAATATCGACTACTGCATAAACAAACGACTGCTTTTCCTGTCTCTT  
ATGGCTGACCTTATGTATTCTTGAAACTAGGAGATCCCTTCCCATTCTCAGCCAA  
AACATGGGATCTTATCCATAGAACAGCTCATCAGCCGGTTGGTGTATTGGAGTGA  
CTC  
ATGGCTCTTCTTGATTTGGCTGTCAACTGCCATACACTACATGTCTTACTCCT  
CAGGAATGTGACTGACACGGATATTCTAGCCCTGGAACGGCGACTGCTGCAA  
ACCATGGATA  
TGATCATAAGCAAAAAGAAAAGGATGGCAATGGCACGGAGAACATGTT  
CAGAAGGGGAA  
GTGCATAACAAACCATCAGTTCTGGGAATGATAAAAAGTGT  
TACCACTCAGCATCAGG  
AAGTGA  
AAATCTTACTCTTATTCAACAGGAAGTGGATGCTTGGAAAGAATTAAGCAGGCAGC  
TTTCTGAAACAGCTGATCTATGCTACCAAGGAGAGAACATGAA  
ACTCCAAA  
ACCTTC  
AAGGGGAAATATTTAATTTCTTGGTACTTTCTCTATTACTGTGTTGGAAAATTT  
CATGGCTACCATCAATATTGTTTGATCGAGTTGGAAAACGGATCCTGTCACAAGAGGCA  
TTGAGATCACTGTGAATTATCTGGGAATCCAATTGATGTGAAGTTGGT  
CCAAACACATT  
TCCTTCATTCTTGTGGAATAATCATCGTCACATCCATCAGAGGATTGCTGATCA  
CTCTTAC  
CAAGTTCTTTATGCCATCTAGCAGTAAGCCTCCAATGTCATTG  
CCTGCTATTAGCAC  
AGATAATGGCATGTACTTTGTCTCCTCTGTGCTGATCCGAATGAGTATGC  
CTTAGAA  
TACCGCACCATAATCACTGAAGTCCTGGAGAACTGCAGTTCAACTCTATC  
ACCCTGGTT  
TGATGTGATCTTCTGGTCAGCGCTCTCTAGCATACTCTTCTATTGGCT  
CACAAAC  
AGGCACCAGAGAACCAAATGGCACCTTGAACTTAAGCCTACTACAGACTGTTAGAGGCCAGT  
GGTTCAAAATTTAGATATAAGAGGGGGAAAATGGAACCAGGGCCTGACATT  
TATAAAC  
AAACAAAATGCTATGGTAGCATTTCACCTTCATAGCATACTCCT  
CCCCGT  
CAGGTGATA  
CTATGACCATGAGTAGCATGCCAGAACATGAGAGGGAGAACTAA  
CTCAAGACAA  
GCAGAGAGCATCCGTGGATATGAGGCTGGTAGAGGGCGGAGAGGCCAAGAA  
ACTAA  
AGGTGAAAATACACTGGAAC  
CTGGGGCAAGACATGTCTATGGTAGCTGAGGCCAAACACGT  
AGGATT  
CCGTTAAGGTT  
CACATGGAAAAGGTT  
TAGCTTGCCTTGAGATTGACTCATT  
AAAATCAGAGACTGTAAC  
AAAAAAAAAAAAAGGGCGGCCGACTCTAGAGTCG  
ACCTGCAGAAGCTTGGCCGCATGGCCAACTTGT  
TTATTGCAGCTTATAATG

## FIGURE 173

MSFLIDSSIMITSQLFFGFWLFFMRQLFKDYEIRQYVVQVIFSVDFAFSCTMFELIIFEI  
LGVLNSSSRYFHWKMNLCVILLILVFMPFYIGYFIVSNIRLLHKQRLLFSCLLWLTMYFF  
WKLGDPPILSPKHGILSIEQLISRVGVIGVTLMALLSGFGAVNCPTYMSYFLRNVTDI  
LALERRLLQTMDMIISKKRMAMARRTMFQKGEVHNKPSPFWGMIKSVTTSASGSENLTLIQ  
QEVDALEELSRLQLFLETADLYATKERIEYSKTFKGKYFNFLGYFFSIYCVWKIFMATINIVF  
DRVVKTDPVTRGIEITVNYLGIQFDVKFWSQHISFILVGIIIVTSIRGLLITLTKFFYAISS  
SKSSNVIVLLLAQIMGMYFVSSVLLIRMSMPLYRTIITEVLGELQFNFYHRWFDVIFLVSA  
LSSILFLYLAHKQAPEKQMAP

**Important features:**

**Signal peptide:**

amino acids 1-23

**Potential transmembrane domains:**

amino acids 37-55, 81-102, 150-168, 288-311, 338-356, 375-398,  
425-444

**N-glycosylation sites.**

amino acids 67-70, 180-183 and 243-246

**Eukaryotic cobalamin-binding proteins**

amino acids 151-160

## **FIGURE 174**

CATGGGAAGTGGAGCCGGAGCCTCCTACACTCGCCATGAGTTCCCTCATCGACTCCAGCA  
TCATGATTACCTCCNGANACTATTTTTGGATTTGGGTGGCTTTCTCNGCGCCAATGTT  
TAAAGACTATGAGATACTGTCAGTATGTTGACNGGTGATCTCTCCGTGACGTTGCCATT  
CTTGCACCATGTTGAGCTCATCTTGAAATCTNGGAGTATTGAATAGCAGCTCCGT  
TATTTCACTGGAAAATGAACCTGTGTGTAATTCTGCTGATCCTGGTTNTCATGGTGCCTT  
TTACATTGGCTATTTATTGTGAGCAATATCCGACTACTGCATAAACAAACGACTGCTTTT  
CCTGTCTCTTATGGCTGACCTTATGTATTTCCAG

## **FIGURE 175**

GTGTTGCCCTGGGGAGGGGAAGGGGAGCCNGGCCCTTCCTAAAATTGCCAAGGGTTTC  
TTTNTTGAATTCCGGGTTNNGNATACCTTCCCAGAAAATATTTTGAGTTGGGTAGNTT  
TTTTCATGCGCCAATTGTTAAAGACTATGAGATACTGTCAGTATGTTGTACAGGTGATNTT  
NTCCGTGACGTTGCATTTCTGCACCATGTTGAGCTCATCATNTTGAAATNTTAGGAG  
TATTGAATAGCAGCTCCGTTATTTCACTGGAAAATGAACCTGTGTGAATTCTGCTGATC  
CTGGTTTCATGGTGCCTTTACATTGGCTATTTATTGTGAGCAATATCCGACTACTGCA  
TAAACAACGACTGCTTTCTGTCTNTTATGGCTGACCTTATGTATTNTNTGGAAAN  
TAGGAGATCCCTTCCCATTCTC

## **FIGURE 176**

CTCGCGCAGGGATCGTCCCATGGCCGGGCTCGGAGCCCGCACCCTTGGGGGCTCCGGGATTGCTACCTTT  
TGGCTCCCTGCTCGA**ACTGCTCTCTCACGGCTGTGCC**TTCAATCTGGACGTATGGTGCTGC  
GGAGGGCGAGCCAGGCAGCCTTCGGCTCTGTGGCCTGCACCGCAGTGCAGCCCCAACCCAGAGCTG  
GCTGCTGGTGGTGCTCCCCAGGCCCTGGCTCTGGCAGCAGCGAATCGCACTGGAGGCCTTCGCTTG  
CCCCTGAGCTGGAGAGACTGACTGCTACAGAGTGGACATCGACAGGGAGCTGATATGCAAAGGAAAGCAA  
GGAGAACCAGTGGTTGGGAGTCAGTGGAGCCAGGGCCTGGGCAAGATTGTTACCTGTGCACACCGATA  
TGAGGCAAGGCAGCAGTGGACCAGATCCTGGAGACGCCGGATATGATTGGTCGCTTGTGCTCAGCCAGGA  
CCTGGCATCCGGATGAGTTGGATGGGAAATGGAAGTTCTGTGAGGGACGCCCAAGGCCATGAACAATT  
TGGTTCTGCCAGCAGGCCACAGCTGCCCTCTCCCTGATAGCCACTACCTCCTCTTGGGCCCCAGGAAC  
CTATAATTGGAAGGGCACGCCAGGGTGGAGCTCTGTGCACAGGGCTCAGCGGACCTGGCACACGG  
TCCCTACGAGGGGGGGAGAGAAGGAGCAGGACCCCCGCCATCCGGTCCCTGCCAACAGCTACTTGGCTT  
CTCTATTGACTCGGGAAAGGTCTGGTGCCTGCAGAAGAGCTGAGCTTGAGCTGGAGGCCCGCCAACCA  
CAAGGGTGTGTTGATCCCTGCAGGACAGCGCAGTCGCTGGCCAGGTTATGCTGTCTGGGAGCG  
CCTGACCTCCGGTTGGCTACTCACTGGCTGTGGCTGACCTCAACAGTGTGATGGCTGCCAGACCTGATAGTGGG  
TGCCCCCTACTTCTTGAGCGCAAGAAGAGCTGGGGTGCTGTGATGTGACTTGAACCAGGGGGTCACTG  
GGCTGGGATCTCCCTCTCCGGCTCTGGCTCCCTGACTCCATGTTGGGATCAGCCTGGCTGTCTGGGGA  
CCTCAACCAAGATGGCTTCCAGATATTGCACTGGGGTGCCTTGTGATGGGAAAGTCTTACATCACCA  
TGGGAGCAGCTGGGGGTGCGGAAACCTCACAGGTGCTGGAGGGCGAGGCTGTTGGGATCAAGAGCTTCGG  
CTACTCCCTGTCAGGAGCTGGATATGGATGGGAACCAATACCTGACCTGCTGGTGGGCTCCCTGGCTGACAC  
CGCAGTGCCTTCAGGGGAGACCCATCCTCCATGAGGCTCTATTGCTCCACGAAGCATCGACCT  
GGAGCAGGCAACTGTGCTGGGGCACTCGGTCTGTGGACCTAAGGGTCTGTTCACTACATTGCACTCCC  
CAGCAGCTATAGCCCTACTGTGGCCCTGGACTATGTGTTAGATGCGACACAGACGGAGGCTCCGGGCCAGGT  
TCCCCGTGTGACCTGAGCTGGAGACGCCATGTTCCAGCTCCAGGAAAATGTCAAAGACAAGCTTGGGCCATTGT  
AGTGACCTTGTCCCTACAGTCTCCAGACCCCTCGGCTCCGGCGACAGGCTCTGGCCAGGGCTGCCAGTGGC  
CCCCATCCTCAATGCCACAGCCCAGCACCCAGGGCAGAGATCCACTTCCTGAAGCAAGGCTGGTGAAGA  
CAAGATCTGCCAGAGCAATCTGCACTGGTCCACGCCGCTCTGTACCCGGGTGAGCAGCACCGAATTCCAACC  
TCTGCCCATGGATGTGGATGGAACAACAGCCCTGTTGACTGAGTGGGAGCCAGTCATTGGCTGGAGCTGAT  
GGTCACCAACTGCCATCGGACCCAGGCCAGGGCTGATGGGATGATGCCATGAAGCCAGCTCCTGGT  
CATGCTTCTGACTCACTGCACTACTCAGGGGTCGGGCCCTGGACCTGCGGAGAAGCCACTCTGCCGTCAA  
TGAGAATGCCCTCCATGTTGAGTGTGAGCTGGGAACCCATGAAGAGAGGTGCCAGGTACCTTCTACCTCAT  
CCTTAGCACCTCGGGATCAGCATTGAGACCACGGAACTGGAGGTAGAGCTGCTGTTGGCACGATCAGTGAGCA  
GGAGCTGCATCCAGTCTGCACTGGAGCCCGTGTCTCATGAGCTGCCACTGTCCTTGAGGAATGCCATTCC  
CCAGCAACTCTCTCTGGTGTGGAGGGCGAGAGAGGCCATGCACTGAGCTGGGATGTGGGAGCAAGGT  
CAAGTATGAGGTCAAGGTTCCAACCAAGGCCAGTCGCTCAGAACCCCTGGCTCTGCCCTTCTCAACATCATGTG  
GCCCTCATGAGATTGCAATGGGAAGTGGTTGCTGATCCCAATGCACTGGAGGTGGAGCAGTGGAGCTAGGGATAGG  
GCAGAAAGGGCTTGCTCTCCAGGCCAACATCCTCCACCTGGATGAGCAGTGGAGCTGGGAGGAGGGCAGGGCCTGG  
GCTGGAGGCCACTGAGCAGCAGGAGCCTGGTGAAGCGGAGGGAGCCAGCATGCTCTGGTGGCCAGTGTCTCTGC  
TGAGAAGAAGAAAACATCACCCCTGGACTGCGCCGGGACGGCAACTGTGTTGAGCTGCTGCCACTCTA  
CAGCTTGACCGCGGGCTGTGCTGCACTGTCATGTCATGGGCCACTCAGTGAAGTCTCCATAAAAGAACATTGATGCTCGAGA  
TGCCTCCACAGTGTACCCAGTGTGATGGTATACTGGACCCATGGCTGTGGTGGCAGAAGGAGTGCCCTGGTGGGT  
CATCCTCCTGGCTGTACTGGCTGGCTGGCTAGCACTGCTGGTGTGCTCCCTGTGGAAGATGGATTCTT  
CAAACGGCGAAGCACCCGAGGCCACCGTGCCCACTGACCTGCGGTGAAGATTCTCGGAAAGACCCAGCAGCA  
GTTCAAGGAGGAGAAGACGGGACCCATCCTGAGGAACAACTGGGGCAGCCCCGGGGAGGGCCGATGCA  
CCCCATCCTGGCTGCTGACGGCATTCCGAGCTGGCCCCGATGGGCATCCAGGGCAGGCCAGGTTCC  
CATGCTCCAGCCTGGCTGTGGCTGCCCTCCATCCCTCCAGAGATGGCTCTGGGATGAGAGGGTAGAGT  
GGGCTGCTGGTGTGCACTCAAGATTGGCAGGATCGGCTCTCTCAGGGCAGAGACCTCTCCACCCACAAGAAC  
TCCTCCCACCCAACTTCCCTTAGAGTGTGAGATGAGAGTGGGAAATCAGGGACAGGGCATGGGTAGGG  
TGAGAAGGGCAGGGTGTGCTGATGCAAAGGTGGGAGAAGGGATCTAATCCCTCTCCATTACCCCTGT  
GTAACAGGACCCAAAGGACCTGCCCTCCCGGAAGTGCCTAACCTAGAGGGTGGGGAGGGTTGTCAGTGA  
CTCAGGCTGCTCTCTAGTTCCCTCTCATCTGACCTTAGTTGCTGCCATCAGTCTAGTGGTTCTGTG  
TTCGTCTATTAAAAAATATTGAGAACAAAAAAAAAAAAAA

## FIGURE 177

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA55737

><subunit 1 of 1, 1141 aa, 1 stop

><MW: 124671, pi: 5.82, NX(S/T): 5

MAGARSRDPWGASGICYLFGSLLVELLFSRAVAFNLDVMGALRKEGEPGSLFGFSVALHRQL  
QPRPQSLLVGAPQALALPGQQANRTGGLFACPLSLEETDCYRVDIDQGADMQKESKENQWL  
GVSVRSQGPGGKIVTCAHRYEARQRVDQILETRDMIGRCFVLSQDLAIRDELDGGEWKFC  
RPQGHEQFGFCQQGTAAGSPDHSYLLFGAPGTYNWKGATARVELCAQGSADLAHLDGPYEA  
GGEKEQDPRLIPVPANSYFGFSIDSGKGLVRAEELSFVAGAPRANHKGAVVILRKDSASRLV  
PEVMLSGERLTSGFGYSLAVADLNSDGWPDLIVGAPYFFERQEELGAVVYVLNQGHHWAGI  
SPLRLCGSPDSMFGISLAVLGDLNQDGFPDIAVGAPFDGDGKVFYHGSSLGVVAKPSQVLE  
GEAVGIKSFYGSLSGSLDMDGQNQYPDLLVGSLADTAVLFRARPILHVSHEVIAPRSIDLEQ  
PNCAGGHSVCVDLRVCFSYIAVPSSYPTVALDYVLDADTDRLRGQVPRVTFLSRNLEEPK  
HQASGTWVWKHQHDRVCGDAMFQLQENVKDKLRAIVVTLSYSLOTPRLLRRQAPGQGLPPVAP  
ILNAHQPSTQRRAEIHFQKQGCEDKICQSNLQLVHARFCTRVSDETFQPLPMDVDGTTALFA  
LSGQPVIGLELMVTNLPSPDAQPQADGDDAHEAQQLLVMLPDSLHYSGVRALDPAEKPLCLSN  
ENASHVECELGNPMPKRGQAQVTFYLILSTSGISIETTELEVELLATISEQELHPVSARARVF  
IELPLSIAGMAIPQQLFFSGVVRGERAMQSERDVGSKVYEVTVSNQGQSLRTLGS AFLNIM  
WPHEIANGKWLLYPMQVELEGGQGPGQKGLCSPRNILHLDVDSRDRRRRELEPPEQQEPGE  
RQEPMSSWWPVSSAEKKNITLDCARGTANCVFSCPLYSFDRAAVLHWGRLWNSTFLEEY  
SAVKSLEVIIVRANITVKSSIKNMLRDASTVIPVMVYLDPMMAVVAEGVPWWVILLAVLAGLL  
VLALLVLLWKMGFFKRKHPEATVPQYHAVKI PREDRQQFKEEKTGTILRNNWGS PRREGP  
DAHPIAADGHPELGPDPGHPGPGTA

**Important features:**

**Signal peptide:**

amino acids 1-33

**Transmembrane domain:**

amino acids 1040-1062

**N-glycosylation sites.**

amino acids 86-89, 746-749, 949-952, 985-988 and 1005-1008

**Integrins alpha chain proteins.**

amino acids 1064-1071, 384-408, 1041-1071, 317-346, 443-465, 385-  
407, 215-224, 634-647, 85-99, 322-346, 470-479, 442-466, 379-408  
and 1031-1047

## **FIGURE 178**

CGCGCCGGCGCAGGGAGCTGAGTGGACGGCTCGAGACGGCGCGTGCAGCAGCTCCAGA  
AAGCAGCGAGTTGGCAGAGCAGGGCTGCATTCCAGCAGGAGCTGCGAGCACAGTGCTGGCT  
CACAACAAGATGCTCAAGGTGTCAGCGTACTGTGTGTGCAGCCGCTGGTGCAGTC  
GTCTCTCGCAGCTGCCCGGGTGGCTGCAGCCGGGGCGGTCGGACGGCGTAATTTCT  
TGGATGATAAACAAATGGCTACCAACAAATCTCTCAGTATGACAAGGAAGTCGGACAGTGGAAC  
AAATTCCGAGACGAAGTAGAGGGATGATTATTCGCACCTGGAGTCCAGGAAAACCCTTCGA  
TCAGGCTTAGATCCAGCTAAGGATCCATGCTAAAGATGAAATGTAGTCGCCATAAAAGTAT  
GCATTGCTCAAGATTCTCAGACTGCAGTCTGCATTAGTCACCGGAGGCTTACACACAGGATG  
AAAGAACAGGAGTAGACCATAGGCAGTGGAGGGTCCCATATTATCCACCTGCAAGCAGTG  
CCCAGTGGTCTATCCCAGCCCTGTTGTGGTTAGATGGTACACTACTCTTTCAGTGCA  
AACTAGAATATCAGGCATGTGCTTAGGAAAACAGATCTCAGTCAAATGTGAAGGACATTGC  
CCATGTCCTCAGATAAGCCCACCAAGTACAAGCAGAAATGTTAAGAGAGCATGCAGTGACCT  
GGAGTTCAGGGAAGTGGCAAACAGATTGCGGACTGGTTCAAGGCCCTCATGAAAGTGGAA  
GTCAAACAAAGAACAAAAACATTGCTGAGGCCTGAGAGAACAGATTGATACCAGCATT  
TTGCCAATTGCAAGGACTCACTGGCTGGATGTTAACAGACTTGATACAAACTATGACCT  
GCTATTGGACCAGTCAGAGCTCAGAACATACAGTTAACATGAAACAGTGATGACCAAGG  
CATTCTCAATTCTGTGACACATACAGGACAGTTAACATGAAACAGTGATGAC  
TGCTTCCAGAGACAGCAAGACCCACCTGCCAGACTGAGCTCAGCAATATTGAGAAGCGGCA  
AGGGTAAAGAACAGCTCTAGGACAGTATATCCCCCTGTGTGATGAAGATGGTTACTACAAGC  
CAACACAATGTCATGGCAGTGGACAGTGCTGGTGTGTTGACAGATATGAAAGTC  
ATGGGATCCAGAATAATGGTGTGAGATTGCTATAGATTTGAGATCTCCGGAGATTT  
TGCTAGTGGCGATTTCATGAATGGACTGATGATGAGGATGATGAAGACGATATTGAAATG  
ATGAAGATGAAATTGAAGATGATGATGAAGATGAAGGGATGATGATGATGGTGGTGTGAC  
CATGATGTATAACATTTGATTGATGACAGTTGAAATCAATAAAATTCTACATTCTAAATT  
CAAAATGATAGCCTATTAAAATTATCTTCTTCCAAATAACAAATGATTCTAAACCTCA  
CATATATTGTATAATTATTGAAAAATTGCAAGCTAAAGTTATAGAAACTTTATGTTAAAT  
AAGAACATTTGCTTGAGTTTATATTCTTACACAAAAAGAAAATACATATGCACTCTA  
GTCAGACAAAATAAGTTGAAGTGCTACTATAATAAAATTTCACGAGAACAAACTTGT  
AAATCTTCCATAAGCAAAATGACAGCTAGTGCTGGATCGTACATGTTAATTTTGAAAG  
ATAATTCTAAGTGAATTTAAAATAAAATTGACCTGGGTCTTAAGGATTTAGG  
AAAAATATGCATGCTTAATTGCATTCCAAAGTAGCATCTGCTAGACCTAGATGAGTCAG  
GATAACAGAGAGATACCACATGACTCCAAAAAAAAAAAAAA

## **FIGURE 179**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49829
><subunit 1 of 1, 436 aa, 1 stop
><MW: 49429, pI: 4.80, NX(S/T): 0
MLKVSAVLCVCAAWSQSLAAAAAVAAAGGRSDGGNFLDDKQWLTTISQYDKEVGQWNKFR
DEVEDDYFRTWSPGKPFQALDPAKDPCLMKCSRHKV рIAQDSQTAVCISHRRLTHRMKEA
GV DHRQWRGPILSTCKQCPVVYPSPVCGSDGHTYSFQCKLEYQACVLGKQISVKCEGHCP
SDKPTSTS RNVKRACSDLEFREVANRLRDWFKA LHESGSQNKTKTLLRPERSRFDT S I LP
CKDSL GWMFNRLDTNYDLLL DQSELRSIYLDKNEQCTKAFFNSCDTYKDSLISNNEWCYCFQ
RQQDPPCQTELSNIQKRQGVKKLLGQYIPLCDEDGYYKPTQCHGSVGQCWCVDRYGNEVMGS
RINGVADCAIDFEISGDFASGDFHEWTDDDEDDIMNDEDEIEDDDEDEGDDDDGGDDHDVYI
```

**Important features:**

**Signal peptide:**

amino acids 1-16

**Leucine zipper pattern.**

amino acids 246-267

**N-myristoylation sites.**

amino acids 357-362, 371-376 and 376-381

**Thyroglobulin type-1 repeat proteins**

amino acids 353-365 and 339-352

## **FIGURE 180**

CAGACTCCAGATTCCCTGTCAACCACGAGGAGTCCAGAGAGGAAACGCCGGAGCGGAGACAACAGTACCTGACGC  
CTCTTCAGCCGGGATGCCCGCAGCAGGGATGGCACAAGATCTGGCTGCCCTCCCCGTGCTCCCTGGCC  
GCTCTGCCCTCCGGTCTGCTGCCCTGGGGCGGCCGGCTTCACACCTCCCTCGATAGCAGTTCACCTTACCCCT  
CCCGCCGGCCAGAAGGAGTGCTCTACAGCCCATGCCCTGAAGGCCCGCTGGAGATCGAGTACCAAGTTTA  
GATGGAGCAGGATTAGATATTGATTTCCATCTTGCTCTCCAGAAGGCAAAACCTTAGTTGAACAAAGAAAA  
TCAGATGGAGTTACACTGTAGAGACTGAAGTTGGTATTACATGTTCTGCTTGACAATACTCAGCACCATT  
TCTGAGAAGGTGATTTCTTGAATTAACTCTGGATAATATGGAGAACAGGCACAAGAACAGAACAGATTGGAAG  
AAATATATTACTGGCACAGATATACTGGATATGAAACTGGAAGACATCTGGAACTCAACAGCATCAAGTCC  
AGACTAACAGCAAAGTGGGCACATACAAATTCTGCTTAGAGCATTGAAGCTCGTGTGAAACATACAAGAAC  
AACTTGATAGAGTCATTCTGGCTATGGTTAATTAGTGGTCACTGGTGGTGTGAGCCATTCAAGTTAT  
ATGCTGAAGAGTCTGTTGAAGATAAGAGGAAAGTAGAACATTAAAACACTAGAGTACGTAACATTGAA  
AATGAGGCATAAAATGCAATAACTGTTACAGTCAAGACCATTAAATGGTCTTCCAAAATATTTGAGATATA  
AAAGTAGGAAACAGGTATAATTAAATGTGAAATTAAAGTCTTCACTTCTGTGCAAGTAATCCTGCTGATCCAG  
TTGTAAGTGTGAAACAGGAATTGGCAGAATATAGGTTAACTGAATGAAGCCATTAAACTGCA  
TTTCTTAACCTTGAAAATTTGCAATGTCTTAGGTGATTAAATAGTGTGAAACACC  
AGTCTGTTTAAACAGGTTCTATTACCCAGAACCTTTTGTAATGCCAGTTACAAATTAAACTGTGGAAGTT  
TCAGTTTAAGTTATAACCTGAGAATTACCTAATGATGGATTGAAATACTTCTAGACTACAAAGCCAA  
CTTTCTCTATTACATATGCATCTCCTATAATGTAATAGATAATAGCTTGTAAATACAATTAGGTTTTG  
AGATTTTATAACCAAATACATTCTAGTGTAAACATATTAGCAGAACGATTAGTCTTGTACTTTGCTTACATT  
CCAAAGCTGACATTTCACGATTAAAAACACAAAGTTACACTTACTAAATTAGGACATGTTCTTCT  
AAATGAAGAATATAGTTAAAGCTTCTCCATAGGGCACATTCTTAACCTTAACAAAGTGTAGGA  
TTTAAATTAATGTGAGGTTAAAGTTAATAGTATCTGTCAAGTTAATATCTGCAACAGTTAA  
TAATCATGTTATGTTAATTAAATGATTGCTGACTTGATAATTCTTACCGCAGTTATGAGGAAATA  
TTGCTAAATGATCTGGGCTTACCCATAAAATATCTCTTCTGAGCTTAAGAATTATCAGAAAACAGGAA  
AGAATTAGAAAACCTGAGAACCTTAATCAAAATAAAATTCACTTAAGTAGAACTATAAATAATATCTAGA  
ATCTGACTGGCTCATGACATCTACTCATAACATAAACTAAAGGAGATGATTAATTTCAGTTAGCTGGAAG  
AAACTTGGCTGTAGGTTTATTTCTACAAGAATTCTGGTTGAATTATTTGTAAGCAGGTACATTATA  
AAATGTAAGCCTACTGTAAAGGTTAGCACTGGGTGACATATTAAATTTTATTATAACAACCTTAT  
TAAATGGCCTTCTGAAACACTTATTGATGTTGAAGTAGGATTAGAAACATAGACTCCCAGTTAA  
CACCTAAATGTGAATAACCCATATACAAACAAAGTTCTGCCATCTAGCTTTGAAGTCTATGGGGCTTAC  
TCAAGTACTAGTAATTAACTTCATCATGAATGAACATAATTAACTTAAAGTTATGCCATTATAACGTTGTTAT  
GACTACATTGTGAGTTAGAAACAAACTAAATTTGGGGTATAGAACCCCTCAACAGGTTAGTAATGCTGGAATT  
CTGATGAGCAATAATGATAACCAGAGAGTGTTCATTACACTCATAGTAGTATAAAAGAGATACTTCCC  
TCTTAGGCCCTGGGAGAAGAGCAGTTAGATTCCCTACTGCCAGGTTTAAATGAGGTAATGCCGTAT  
ATGATCAATTACCTTAATGGCAAGAAAATGTTCTCAGGTGTCTAGGGTATCTCTGCAACACTTGCGAGAACAA  
AGGTCAATAAGATCCTGGCTATGAATACCCCTCCCTTGGCTGTTAAATTGCAATGAGAACAAATTACA  
GTACCCATAACTAAACAGCAGGTACAGATAAAACTACTGCACTCTTCTTACAAATGAAATTGTTACATACTTCT  
CCTCCTGTATGGCTGTACTGTACTCTGACTCCCTTACAAATGAAATTGTTACATACTTCT  
ACATGTATGATTGCTTACCTGATCTTAAACCTATGATTGACTCTTACCTATGAAAGTAAAGAACGATAATTGCTT  
TATTGGAAAAGAATTAGGAATACTAAGGACAATTATTGTTATAGACAAGTAAAGAACAGATATTAAAGG  
CATAAACAAAAAGCAAACCTGTAAACAGAGTAAAGAACAGATATTCTAAAGACATACTGTTATCTGCTT  
CATATGCTTTTTAATTCACTATCCATTCTAAATTAAAGTTATGCTAAATTGAGTAAGCTGTTATCACTT  
AACAGCTATTGCTTTCAATATAACAAATTAAACTACAATTAACTAAGGCCAACCGATTTC  
CATATGTAGCAGTTACCGTGTTCACCTCACACTAAGGCCAGTGGTTGCTCTGATATGCAATTGGATGATTAAT  
GTTATGCTGTTCTTCTGATGTGAATGTCAAGACATGGAGGGTGTGTAATTGTTATGGAAAATTAAATCCTTCTA  
CACATAATGGGTCTTAAATTGACAAAAATGAGCACTTACAATTGTTATGCTCCTCAAATGAAGATTCTTAT  
GTGAAATTAAAAGACATTGATTCCGATGTAAGGATTTCATGTAAGTACAATAATGCAACATCAGTGTG  
CTCAAACGTCTTATACTTATAAACAGCCATCTTAAATAAGCAACGTATTGTGAGTACTGATATGTATATAATA  
AAATTATCAAAGGAAAA

## **FIGURE 181**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52196
><subunit 1 of 1, 229 aa, 1 stop
><MW: 26017, pI: 4.73, NX(S/T): 0
MGDKIWLPPVLLAALPPVLLPGAAGFTPSSLSDFTFTLPAGQKECFYQPMPLKASLEIEY
QVLDGAGLDIDFHLASPEGKTLVFEQRKSDGVHTVETEVGDYMFCDNTFSTISEKVIFFEL
ILDNMGEQAQEQQEDWKKYITGTDILDLMKLEDILESINSIKSRLSKSGHIQILLRAFEARDRN
IQESNFDRVNFWSMVNLVVVVSAIQVYMLKSLFEDKRKSRT
```

**Important features:**

**Signal peptide:**

amino acids 1-23

**Transmembrane domain:**

amino acids 195-217

**N-myristoylation site.**

amino acids 43-48

**Tyrosine kinase phosphorylation site.**

amino acids 55-62

## **FIGURE 182**

CCATCCCTGAGATCTTTATAAAAAACCCAGTCTTGCTGACCAGACAAAGCATACCAAGAT  
CTCACCAAGAGAGTCGCAGACACTATGCTGCCTCCATGCCCTGCCAGTGTGTCCTGGATG  
CTGCTTCCTGCCTCATTCTCCTGTGTCAGGTTCAAGGTGAAGAAACCCAGAAGGAAC TGCC  
CTCTCCACGGATCAGCTGTCCAAAGGCTCCAAGGCCTATGGCTCCCCCTGCTATGCCTTGT  
TTTGTACCAAAATCCTGGATGGATGCAGATCTGGCTTGCCAGAAGCGGGCCCTCTGGAAAAA  
CTGGTGTCTGTGCTCAGTGGGCTGAGGGATCCTCGTGTCCCTGGT GAGGAGCATTAG  
TAACAGCTACTCATACATCTGGATTGGCTCCATGACCCCACACAGGGCTTGAGCCTGATG  
GAGATGGATGGAGTGGAGTAGCACTGATGTGATGAATTACTTTGCATGGAGAAAAATCCC  
TCCACCATCTAAACCCCTGGCCACTGTGGGAGCCTGTCAAGAACGACAGGATTCTGAAGTG  
GAAAGATTATAACTGTGATGCAAAGTTACCCATGTCTGCAAGTTCAAGGACTAGGGCAGGT  
GGGAAGTCAGCAGCCTCAGCTGGCGTGCAGCTCATGGACATGAGACCAGTGTGAAGAC  
TCACCCCTGGAAGAGAATATTCTCCCCAAACTGCCCTACCTGACTACCTTGT CATGATCCTCC  
TTCTTTTCTTTCTTCACCTCATT CAGGCTTTCTGTCTTCCATGTCTTGAGATC  
TCAGAGAATAATAATAAAAAATGTTACTTTATAAAAAAAAAAAAAAAA

## **FIGURE 183**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56965
<subunit 1 of 1, 175 aa, 1 stop
<MW: 19330, pI: 7.25, NX(S/T): 1
MLPPMALPSVSWMLLSCLILLCQVQGEETQKELPSPRISCPKGSKAYGSPCYALFLSPKSWM
DADLACQKRPSGKLVSVLSGAEGSFVSSLVRSISNSYSYIWIGLHDPTQGSEPDGDGWEWSS
TDVMNYFAWEKNPSTILNPGHCGSLSRSTGFLWKDYNCDAKLPYVCKFKD
```

**Important features:**

**Signal peptide:**

amino acids 1-26

**C-type lectin domain signature.**

amino acids 146-171

## **FIGURE 184**

CCAGTCTGTCGCCACCTCACTGGTGTCTGCTGTCCCCGCCAGGCAAGCCTGGGTGAGAGC  
ACAGAGGAGTGGGCCGGGACCATGCGGGGGACGCGGCTGGCGCTCCTGGCGCTGGTGC  
TGCCTGCGGAGAGCTGGCGCCGGCCCTGCGCTGCTACGTCTGTCCGGAGCCCACAGGAGTGT  
CGGACTGTGTCACCATGCCACCTGCACCAACGAAACCATGTGCAAGACCACACTCTAC  
TCCCGGGAGATAGTACCCTTCCAGGGGACTCCACGGTGACCAAGTCCTGTGCCAGCAA  
GTGTAAGCCCTCGGATGTGGATGGCATCGGCCAGACCCCTGCCGTGCTGCAATACTG  
AGCTGTGCAATGTAGACGGGGCGCCGCTCTGAACAGCCTCCACTGCCGGCCCTCACGCTC  
CTCCCACTCTTGAGCCTCCGACTGTAGGTCCCCGCCACCCCCATGCCCTATGCCGCCA  
GCCCGAATGCCCTGAAGAAGTGCCCTGCACCAAGGAAAAAAAAAAAAAAA

## **FIGURE 185**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56405
<subunit 1 of 1, 125 aa, 1 stop
<MW: 13115, pI: 5.90, NX(S/T): 1
MRGTRLALLALVLAACGELAPALRCYVCPEPTGVSDCVTIATCTTNETMCKTLYSREIVYP
FQGDSTVTKSCASKCKPSDVDGIGQTLPVSCCNTELCNVDGAPALNSLHCGALTLLPLLSLRL
```

**Important features:**

**Signal peptide:**

amino acids 1-17

**N-glycosylation site.**

amino acids 46-49

## **FIGURE 186**

CTGCAGTCAGGACTCTGGGACCGCAGGGGGCTCCGGACCCTGACTCTGCAGCCGAACCGGC  
ACGGTTCTGGGGACCCAGGCTTGCAAAGTGACGGTCATTTCTTTCTCCCTCTT  
GAGTCCTTCTGAGATGATGGCTCTGGGCGCAGCAGGAGCTACCCGGTCTTGTCGCATGG  
TAGCGGCGGCTCTCGCGGCCACCCCTGCTGGGAGTGAGCGCCACCTGAACTCGTTCTC  
AATTCCAACGCTATCAAGAACCTGCCCGCACCGCTGGGCGGCTGCGGGCACCCAGGCTC  
TGCAGTCAGCGCCGCCGGAAATCCTGTACCCGGCGGAATAAGTACCAAGACCATTGACA  
ACTACCAGCCGTACCGTGCAGAGGACGAGGAGTGCGGCAGTGATGAGTACTGCGCTAGT  
CCCACCCGCGGAGGGACGCAGGCGTGCAGGAAATCTGTCTGCCTGCAGGAAGCGCCAAAACG  
CTGCATGCGTCACGCTATGTGCTGCCCGGAATTACTGAAAAATGGAATATGTGTCTT  
CTGATCAAATCATTCCGAGGAGAAATTGAGGAAACCATCACTGAAAGCTTGGTAATGAT  
CATAGCACCTTGGATGGGTATTCCAGAAGAACCACCTTGTCTTCAAAATGTATCACACCAA  
AGGACAAGAAGGTTCTGTTGTCTCCGGTCATCAGACTGTGCCTCAGGATTGTGTTGTGCTA  
GACACTTCTGGTCCAAGATCTGTAAACCTGTCCTGAAAGAAGGTCAAGTGTGTACCAAGCAT  
AGGAGAAAAGGCTCTCATGGACTAGAAATATTCCAGCGTTGTTACTGTGGAGAAGGTCTGTC  
TTGCCGGATACAGAAAGATCACCATAAGCCAGTAATTCTCTAGGCTTCACACTTGTCA  
GACACTAAACCAGCTATCCAAATGCAGTGAACTCCTTTATATAATAGATGCTATGAAAACC  
TTTATGACCTTCATCAACTCAATCCTAAGGATATAAGTTCTGTGGTTCACTTAAGCAT  
TCCAATAACACCTTCCAAAAACCTGGAGTGTAAAGAGCTTGTGTTATGGAACACTCCCTG  
TGATTGCAGTAAATTACTGTATTGAAATTCTCAGTGTGGCACTTACCTGAAATGCAATGA  
AACTTTAATTATTTCTAAAGGTGCTGCACTGCCTATTTCTTCTTGTGTTATGAAATTT  
TTGTACACATTGATTGTTATCTGACTGACAAATATTCTATATTGAACGTAAATCATT  
TCAGCTTATAGTTCTAAAAGCATAACCCCTTACCCATTAAATTCTAGAGTCTAGAACGCA  
AGGATCTTGGAAATGACAAATGATAGGTACCTAAATGTAACATGAAAATACTAGCTTATT  
TTCTGAAATGTAATCTTAATGCTTAAATTATTTCCCTTAGGCTGTGATAGTTTGA  
AATAAAATTAAACATTAAAAAAAAAA

## **FIGURE 187**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57530
<subunit 1 of 1, 266 aa, 1 stop
<MW: 28672, pI: 8.85, NX(S/T): 1
MMALGAAGATRVFVAMVAAALGGHPLLGVSATLNSVLNSNAIKNLPPPLGGAAGHPGSAVSA
APGILYPGGNKYQTIDNYQPYPACAEDEECGTDEYCASPTRGGDAGVQICLACRKRRKRCMRH
AMCCPGNYCKNGICVSSDQNHFREIEETITESFGNDHSTLDGYSRRTTLSSKMYHTKGQEG
SVCLRSSDCASGLCCARHFWSKICKPVLKEGQVCTKHRRKGSHGLEIFQRACYCGEGLSCRIQ
KDHHQASNSSLHTCQRH
```

**Important features:**

**Signal peptide:**

amino acids 1-23

**N-glycosylation site.**

amino acids 256-259

**Fungal Zn(2)-Cys(6) binuclear cluster domain**

amino acids 110-126

## **FIGURE 188**

TGTGTTCCCTGCAGTCAGAATTGGGACNGCAGGGTTCCCGGACCTGATTTGCAGCGGA  
ACGGGAAGGTTTGAGGGACCCAGGTTGAAATGACGGTCATTTTTCTCCTTCNG  
GAGTCCTNTGAGANGATGGTTGGGCGCAGCGGGAGCTAACCGGTTTGTNGCGATG  
GTAGCGCGGTTTCCGGGCCACCTNTGCTGGAGTGAGCGCACCTGAATCGGTTTC  
AATTCCAACGNTATCAAGAACCTGCCACCGNTGGCGCGCTCGGGGCACCCAGGNTT  
TGCAGTCAGCGCCGCCGGAAATCCTGTACCCGGCGGAATAAGTACCAGACCATTGACA  
ATTACCAGCCGTACCCGTGCGCAGAGGACGAGGAGTGCGGCACTGATGAGTACTGCCTAGT  
CCCACCCGCGGAGGGGANGCGGGCGTGC<sub>AA</sub>ATNTGTNTNGCCTGCAGGAAGCGCCGAAAACG  
CTGCATGCGTCANGCTATGTGCTGCCCGGGAAATTACTGCAAAATGGAATATGTGTNTT  
CTGATCAAATCATTCCGAGGAGAAATTGAGGAAACCATCACTGAAAGCTTGGTAATGAT  
CATAGCACCTTGGATGGG

## FIGURE 189

GAGGAACCTACCGTACCGGCCGCGCTGGTAGTCGCCGTGCGCACCTCACCAATCCCGTGCGCCGCGG  
CTGGGCCGTCGGAGAGTCGCGTGTGCTTCTCCTGCACGCCGTGCTGGCTCGGCCAGGCCGGTCCGCC  
GGTTTGAGGATGGGGAGTAGCTACAGGAAGCGACCCCGCATGCCAAGGTATTTTGAAATGAAAAGGA  
AGTATTAGAAATGAGCTGAAGACCATTACAGATTAAATTTGGGAGACAGATTGTGATGCTTGATTCAC  
TGAAGTAATGTAGACAGAAAGTCTCAAATTGCAATTACATCAACTGGAACCGAGCTGAATCTTAATGTT  
TTAACATCAGAACTTGCAATAAGAAAGAAATGGGAGTCTGGTAAATAAGATGACTATATCAGAGACTGAAAAG  
GATCATTCTGTGTTCTGATAGTGATATGCCATTAGGGCACAGATCAGGATTTACAGTTACTTGG  
AGTGTCAAAACTGCAAGCAGTAGAGAAATAAGACAAGCTTCAAGAAATTGGATTGAAGTTACATCTGATAA  
AAACCGAATAACCAAATGCACATGGGATTTAAAAATAATAGAGCATATGAAGTACTCAAAGATGAAGA  
TCTACGGAAAAGTATGACAAATATGGAGAAAAGGGACTGAGGATAATCAAGGTGGCCAGTGAAGACTGG  
CTATTATCGTTATGATTTGGTATTATGATGATGATCCTGAAATCATAACATGGAAAGAAGAGAATTGATGC  
TGCTGTTAATTCTGGAGAACTGTGTTGTAATTAACTCCCCAGGCTGTCACACTGCCATGATTAGCTCC  
CACATGGAGAGACTTGCTAAAGAAGTGGATGGTTACTCGAATTGGAGCTGTAACGTGGTGTGATGATAGAAT  
GCTTGCGAATGAAAGGAGTCACAGCTATCCCAGTCTTCATTTCGGTCTGGATGGCCAGTGAAGATA  
TCATGGAGACAGATCAAAGGAGAGTTAGTGAGTTGCAATGCAGCATGTTAGAAGTACAGTGACAGAACTTTG  
GACAGGAAATTGTCAACTCAAACACTGCTTTGCTGCTGGTATTGGCTGGTGTGACTTTTGTTCAAA  
AGGAGGAGATTGTTGACTTACAGACACGACTCAGGTTAGGGCATGTTCTCAACTCATTGGATGCTAA  
AGAAATATTTGGAAGTAATACATAATCTTCCAGATTGAAACTACTTCCGAAACACACTAGAGGATCGTT  
GGCTCATCATGGTGGCTGTTATTTCATTTGGAAAAAAATGAAATTCAAATGCTGAGCTGAAAGAAACT  
AAAAACTCTACTTAAAGATGATCATATTCAAGTGGCAGGTTGACTGTTCTGACCAGACATCTGAGTAA  
TCTGTTATGTTTCAGCCGCTCTAGCAGTATTAAAGGACAAGGAAACAAAGAATATGAAATTGATCATGGAAA  
GAAGATTCTATATGATATACTTGCTTGTGCAAAGAAAGTGTGAATTCTCATGTTACACGCTGGACTCAAAA  
TTTCTGCCAATGACAAGAACATGGCTGTTGATTCTTGTGCCCCCTGGTGTCCACATGCGAGCTTACT  
ACCAAGAGTTACGAAGAGCATCAAATCTCTTATGGTCAGCTTAAGTTGGTACACTAGATGTACAGTTCATG  
GGGACTCTGTAACATGATAACATTCAAGGTTATCCAACACAGTGGTATTCAACCAGTCCAACATTGAGTA  
TGAAGGACATCACTGCTGAACAAATCTTGAGTTCATAGAGGATCTTATGAATCCTCAGGGTCTCCCTAC  
ACCCACCACCTCAACGAACTAGTTACACAAGAAAACACAACGAAGTCTGGATGGTGATTCTATTCTCCGTG  
GTGTCATCCTTGCCAAGCTTAATGCCAGAATGGAAAAGAATGGCCGGACATTAACGGACTGATCAACGTGG  
CAGTATAGATTGCCAACAGTATCATCTTTGTCGCCAGGAAACGTTCAAAGATAACCTGAGATAAGATTTT  
TCCCCAAAATCAAATAAGCTTACAGTACAGTTACAATGGTIGGAATAGGGATGCTTATTCCCTGAGAAT  
CTGGGGTCTAGGATTTCACCTCAAGTATCCACAGATCTAACACCTCAGACTTCAGTGAAAAGTCTACAAGG  
GAAAATCATGGGTGATTCTATGCTCTGGTGTGGACCTGCCAGAATTGCTCCAGAATTGCTGAGCT  
CTTGGCTAGGATGATTAAGGAAAAGTGAAGCTGGAAAAGTACAGTGTCAAGGCTTATGCTCAGACATGCCAGAA  
AGCTGGATCAGGGCTATCCAACGTTAAAGTTTATTCTACAGAAAGAGCAAAAGAGAATTCTCAAGAAGAGCA  
GATAAATACCAAGAGATGCAAAAGCAATCGCTGCCATTAAAGTGAAAAAGTCTCCGAAATCAAGGCAA  
GAGGAATAAGGATGAACTGATAATGTTACATTATGATGGGAATGAATGAACATTATCTAGACTTGCACTG  
AAGACACCTATTAGAATGTTACATTATGATGGGAATGAATGAACATTATCTAGACTTGCACTG  
GAATTATCTACAGCACTGGTAAAGAAGGGTCTGCAAACATTCTGTAAAGGGCCGTTATAAATATT  
GACTTGCAGGCTATAATATGGTCACACATGAGAACAGTACATGTTCTTGTGTTATTGCT  
TTAACACCTTAAAAAATATTAAACGATTCTAGCTCAGGCCATACAAAGTAGGCTGGATTGAGTCCATG  
GACCATAGATTGCTGTCCTCGACGGACTTAAATGTTCAGGGCTGGCTGAACATGAGTCTGCTGTGCT  
ATCTACATAATGTCTAAGTTGATAAAAGTCCACTTCCCTCACGTTTTGCTGACCTGAAAAGAGGTAAC  
TAGTTTGTCACTGTTCTCTAAAATGCTATCCCTAACCATATATTATTTGCTTTAAAACACCCAT  
GATGTTGACAGTAAACAAACCTGTTATGCTGTATTATTATGAGGAGATTCTCATTGTTCTTCTCTCA  
AAGGTTGAAAATGCTTTAATTTCACAGCCGAGAACAGTGCAGCAGTATATGTCACACAGTAAGTACAC  
AAATTGAGCAACAGTAAGTGCACAAATTCTGAGTTGCTGTATCATCCAGGAAACCTGAGGGAAAAAATT  
TAGCAATTAACTGGGATTGAGGTATCTAAATATGTTATCAAGTATTAGGTTCTATTTAAAGATATA  
TGTGTTCATGTTCTGAAATTGCTTCTAGAAATTCTCCACTGATAGTTGATTGGAGCTCTAATAT  
TTACATATTGCTCTGAACTTGTGTTCTGACCTGATCTTATTACATTGGGTTCTTCTGATAGTTGG  
TTTTCACTCTGTCAGTCTATTATTACAAATGAGAAAATTACTTACAGGTTGTTACTGAGCTTAT  
AATGATACTGAGTTATTCCAGTTACTGAGTTACTGCAAGGGCTGCCCTTCTAGATAAATATTGACATAATA  
ACTGAAGTTATTGTTATAAGAAAATCAAGTATATAATCTAGGAAAGGGATCTCTAGTTCTGTTGTTAGA  
CTCAAGAATCACAAATTGTCAGAACATGAGTTGTTAGTTATAATTCAAGGTTACAGAATGGTAAAATT  
CCAATCAGTCAAAAGAGGTCATGAATTAAAGGCTGCAACTTTCAAAAAAAAAAAAAA

## **FIGURE 190**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56439
<subunit 1 of 1, 747 aa, 1 stop
<MW: 86127, pI: 7.46, NX(S/T): 2
MGVWLNKDDYIRDLKRIILCFLIVYMAILVGTDQDFYSLLGVSKTASSREIRQAFKKLALKL
HPDKNPNNPNAHGDFLKINRAYEVLKDEDLRKKYDKYGEKGLEDNQGGQYESWNYYRYDFGI
YDDDPEIITLERREFDAAVNSGELWFVNFYSPGCSHCHDLAPTRWDFAKEVDGLLRIGAVNC
GDDRMLCRMKGVNNSYPSLFIFRSGMAPVKYHGDRSKESLVSFAMQHVRSTVTELWTGNFVNS
IQTAFAAGIGWLITFCSKGGDC LTSQTRLRLSGMLFLNSLDAKEIYLEVIHNLPDFELLSAN
TLEDRLAHHRWLLFFFHFGKNENSNDPELKKLKTLKNDHIQVGRFDCSSAPDICSNLYVFQP
SLAVFKGQGTKEYEIHGKKILYDILAFAKESVNSHVTTLGPQNF PANDKEPWLVDFFFAPWC
PPCRALLPELRRASNLLYQQLKF GTLDCTVHEGLCNMYNIQAYPTTVFNQSNIHEYEGHHS
AEQILEFIEDLMNPVVSLPTTFNELVTQRKHNEVWMVDFYSPWCHPCQVLMPEWKRMART
LTGLINVGSIDCQQYHSFCAQENVQRYPEIRFFF PKSNKAYQYHSYNGWNRDAYSLRIWGLG
FLPQVSTDLPQTFS EKV LQGKNHWVIDFYAPWCGPCQNFAPEFELLARMIKGKVAGKVDC
QAYAQT CQKAGIRAYPTVKFYFYERAKRN FQEEQINTRDAKAIAALISEKLET LRN QGKR NKDEL
```

**Important features:**

**Endoplasmic reticulum targeting sequence.**

amino acids 744-747

**Cytochrome c family heme-binding site signature.**

amino acids 158-163

**Nt-dnaJ domain signature.**

amino acids 77-96

**N-glycosylation site.**

amino acids 484-487

## **FIGURE 191**

AGACAGTACCTCCTCCCTAGGACTACACAAGGACTGAACCAGAAGGAAGAGGACAGAGCAAA  
GCCATGAACATCATCCTAGAAATCCTCTGCTTCTGATCACCATCATCTACTCCTACTTGG  
GTCGTTGGTGAAGTTTCTTCATTCTCAGAGGAGAAAATCTGTGGCTGGGAGATTGTTCTCA  
TTACTGGAGCTGGGCATGGAATAGGCAGGCAGACTACTTATGAATTGCAAAACGACAGAGC  
ATATTGGTTCTGTGGGATATTAATAAGCGCGGTGGAGGAAACTGCAGCTGAGTGCCGAAA  
ACTAGGCGTCACTGCGCATGCGTATGTGGTAGACTGCAGCAACAGAGAAGAGATCTATCGCT  
CTCTAAATCAGGTGAAGAAAGAAGTGGGTGATGTAACAATCGTGGTGAATAATGCTGGACA  
GTATATCCAGCCGATCTTCTCAGCACCAAGGATGAAGAGATTACCAAGACATTTGAGGTCAA  
CATCCTAGGACATTTGGATCACAAAGCACTTCTTCATCGATGATGGAGAGAAATCATG  
GCCACATCGTCACAGTGGCTTCAGTGTGCGGCCACGAAGGGATTCTTACCTCATCCCATA  
TGTTCCAGCAAATTGCCGCTGTTGGCTTCACAGAGGTCTGACATCAGAACATTCAAGGCCTT  
GGGAAAAACTGGTATCAAAACCTCATGTCCTGCCAGTTTGTAATACTGGGTCACCA  
AAAATCCAAGCACAAAGATTATGGCCTGTATTGGAGACAGATGAAGTCGAAGAAGTCTGATA  
GATGGAATACTTACCAATAAGAAAATGATTTGTTCCATCGTATATCAATATCTTCTGAG  
ACTACAGAACAGTTCTCCTGAACGCGCCTCAGCGATTTAAATCGTATGCAGAACATTCAAT  
TTGAAGCAGTGGTTGCCACAAATCAAATGAATAAAATAAGCTCCAGGCAGAGATG  
TATGCATGATAATGATATGAATAGTTCGAACATGCTGCAAAGCTTATTCACATTTT  
TCAGTCCTGATAATATTAAAAACATTGGTTGGCACTAGCAGCAGTCAAACGAACAAGATTA  
ATTACCTGTCCTCCTGTTCTCAAGAATATTACGTAGTTTCTAGGTCTGTTTCTT  
TCATGCCTCTTAAAAACTCTGTGCTTACATAAACATACTTAAAGGTTCTTAAGATAT  
TTTATTTTCCATTAAAGGTGGACAAAAGCTACCTCCCTAAAGTAAATACAAAGAGAACT  
TATTTACACAGGAAAGGTTAACAGACTGTTCAAGTAGCATTCCAATCTGTAGCCATGCCACAG  
AATATCAACAAGAACACAGAACAGAACATGAGTCACAGCTAACAGAGATCAAGTTCAGCAGGCAGCTT  
ATCTCAACCTGGACATATTAAAGATTAGCATTGAAAGATTTCCCTAGCCTCTTCTT  
TCATTAGCCCCAAACGGTGCAACTCTATTCTGGACTTTATTACTTGATTCTGTCTTGTAT  
AACTCTGAAGTCCACCAAAAGTGGACCCCTCTATATTCCCTTTTATAGTCTTATAAGA  
TACATTATGAAAGGTGACCGACTCTATTAAATCTCAGAACATTAAAGTTCTAGCCCCATGA  
TAACCTTTCTTGTAAATTATGCTTCATATATCCTGGTCCCAGAGATGTTAGACAAT  
TTTAGGCTCAAAATTAAAGCTAACACAGGAAAGGAACGTACTGGCTATTACATAAGAAA  
CAATGGACCCAAGAGAAGAA

## **FIGURE 192**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56409
<subunit 1 of 1, 300 aa, 1 stop
<MW: 33655, pI: 9.31, NX(S/T): 1
MNIIILEILLLITIIYSYLESLVKFFIPQRRKSVAGEIVLITGAGHGIGRQTTYEFAKRQSI
LVLWDINKRGVEETAAECRKLGVTAHYVVDCSNREEIYRSLNQVKKEVGDVTIVVNNAAGTV
YPADLLSTKDEEITKTFEVNILGHFWITKALLPSMMERNHGHIVTVASVCVGHEGIPYLIPYC
SSKFAAVGFHRGLTSELQALGKTGIKSCLCPVFVNTGFTKNPSTRLWPVLETDEVVRSLID
GILTNKKMIFVPSYINIFLRLQKFLPERASAILNRMQNIQFEAVVGHKIKMK
```

**Important features:**

**Signal peptide:**

amino acids 1-19

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 30-33 and 58-61

**Short-chain alcohol dehydrogenase family protein**

amino acids 165-202, 37-49, 112-122 and 210-219

## **FIGURE 193**

CGGGGGCGGCTGCGGGCGCGAGGTGAGGGCGCGAGGTGAGGGCGCGAGGTTCCCAGCAGG  
ATGCCCGGCTCTGCAGGAAGCTGAAGTGAGAGGCCGGAGAGGGCCAGCCGCCGGGGC  
**AGGATGACCAAGGCCGGCTGTCGGCTGTGGCTGGTCTGGTGTTCATGATCCT**  
GCTGATCATCGTGTACTGGACAGCGCAGGCCCGCGACTTCTACTTGCACACGTCTTCT  
CTAGGCCGACACGGGCCGGCTGCCACGCCGGGCCGGACAGGGACAGGGAGCTCACG  
GCCGACTCCGATGTCGACGAGTTCTGGACAAGTTCTAGTGCTGGCGTAAGCAGAGCGA  
CCTTCCCAGAAAGGAGACGGAGCAGCCGCTGCGCCGGGAGCATGGAGGAGAGCGTGAGAG  
GCTACGACTGGTCCCCCGCGACGCCCGCGAGCCCAGACCAGGGCGGCAGCAGGCGGAG  
CGGAGGAGCGTGCTGCGGGCTCTGCGCCAACCTCCAGCCTGGCCTCCCCACCAAGGAGCG  
CGCATTGACGACATCCCCACTCGGAGCTGAGCCACCTGATCGGACGACGGCACGGG  
CCATCTACTGCTACGTGCCAAGGTGGCCTGCACCAACTGGAAGCGCGTGTGATCGTGTG  
AGCGGAAGCCTGCTGCACCGCGGTGCGCCCTACCGCGACCCGCTGCGCATCCGCGGAGCA  
CGTGCACAACGCCAGCGCGCACCTGACCTTCAACAAGTTCTGGCGCGCTACGGGAAGCTCT  
CCCGCCACCTCATGAAGGTCAAGCTCAAGAAGTACACCAAGTTCTCTTGTGCGGACCCCC  
TTCGTGCGCCTGATCTCCGCCCTCCGAGCAAGTTGAGCTGGAGAACGAGGAGTTCTACCG  
CAAGTTGCCGTGCCCATGCTGCGGCTGTACGCCAACACACCAGCCTGCCGCTGGCGC  
GCGAGGCCTCCGCGCTGGCCTCAAGGTGTCTCGCCAACCTCATCCAGTACCTGCTGGAC  
CCGCACACGGAGAAGCTGGGCCCTCAACGAGCACTGGCGGAGGTGTACCGCCTCTGCCA  
CCCGTGCCAGATCGACTACGACTTCGTGGGAAGCTGGAGACTCTGGACGAGGACGCCGCG  
AGCTGCTGCAGCTACTCCAGGTGGACCGCAGCTCCGCTCCCCCGAGCTACCGAACAGG  
ACCGCCAGCAGCTGGAGGAGGACTGGTTGCCAAGATCCCCCTGGCCTGGAGGCAGCAGCT  
GTATAAAACTCTACGAGGCCGACTTTGTTCTTCGGCTACCCCAAGCCCAAAACCTCCTCC  
**GAGACTGAAAGCTTCGCGTTGCTTTCTCGCGTGCCTGGAACCTGACGCACGCGCACTCC**  
AGTTTTTTATGACCTACGATTTGCAATCTGGCTTCTGTTCACTCCACTGCCTCTATCC  
ATTGAGTACTGTATCGATATTGTTTTAAGATTAATATTCAGGTATTAATACGA

## **FIGURE 194**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56112
<subunit 1 of 1, 414 aa, 1 stop
<MW: 48414, pI: 9.54, NX(S/T): 4
MTKARLFRLWLVGSVFMILLIIVYWDSAGAAHFYLHTSFSRPTGPPPLPTPGPDRDRELTA
DSDVDEFLDKFLSAGVKQSDLPRKETEQPPAPGSMEESVRGYDWSPRDARRSPDQGRQQAER
RSVLRGFCANSSLAFPTKERAFDDIPNSELSHLIVDDRHGAIYCYVPKVACTNWKRVMIVLS
GSLLHRGAPYRDPLRIPREHVHNASAHLTFNKFWRRYGKLSRHLMKVKLKKYTKFLFVRDPF
VRLISAFRSKFELENEEFYRKFAVPMLRLYANHTSLPASAREAFRAGLKVSFANFIQYLLDP
HTEKLAPFNEHWRQVYRLCHPCQIDYDFVGKLETLDDEAAQLLQLLQVDRQLRFPPSYRNRT
ASSWEEDWFAKIPLAWRQQLYKLYEADFVLFGYPK PENLLRD
```

**Important features:**

**Signal peptide:**

amino acids 1-31

**N-glycosylation sites.**

amino acids 134-137, 209-212, 280-283 and 370-373

**TNFR/NGFR family cysteine-rich region protein**

amino acids 329-332

## FIGURE 195

TCGGGCCAGAATT CGGCACGAGGC GGAC GAGGC GACGGC CTACGGGCTT GGAGGTGA  
AAGAGGCCAGAGTAGAGAGAGAGAGACCGACGTACAGGGATGGCTACGGAACCGCGCT  
ATGCCGGGAAGGTGGTGGTGTGACC GGGGGCGGGCGCGCATCGGAGCTGGATCGTGC  
GCCTCGTGAACAGCGGGGCCGAGTGGTTATCTGCACAAGGATGAGTCTGGGGCCGGC  
CCTGGAGCAGGAGCTCCCTGGAGCTGTCTTATCCTCTGTGATGTGACTCAGGAAGATGATG  
TGAAGACCTGGTTCTGAGACCATCCGCCGATTGGCCGCTGGATTGTGTTGTCAACAAAC  
GCTGGCCACCACCCACCCCCACAGAGGCCTGAGGAGACCTCTGCCAGGGATTCCGCCAGCT  
GCTGGAGCTGAACCTACTGGGACGTACACCTTGACCAAGCTGCCCTCCCTACCTGCGGA  
AGAGTCAAGGAATGTCATCAACATCTCCAGCCTGGTGGGGCAATCGGCCAGGCCAGGCA  
GTTCCCTATGTGGCACCAAGGGGGCAGTAACAGCCATGACCAAAGCTTGGCCCTGGATGA  
AAGTCCATATGGTGTCCGAGTCAACTGTATCTCCCCAGGAAACATCTGGACCCGCTGTGGG  
AGGAGCTGGCAGCCTTAATGCCAGACCCCTAGGCCACAATCCGAGAGGGCATGCTGCCAG  
CCACTGGGCCGCATGGGCCAGCCCGCTGAGGTGGGGCTGCCAGTGTCCCTGGCCCTCCGA  
AGCCAACCTCTGCACGGCATTGAACTGCTCGTACGGGGGTGCAGAGCTGGGTACGGT  
GCAAGGCCAGTCGGAGCACCCCGTGGACGCCCGATATCCCTCCTTGATTCTCTCATTT  
CTACTTGGGCCCCCTCCTAGGACTCTCCCACCCAAACTCCAACCTGTATCAGATGCAGC  
CCCCAAGCCCTAGACTCTAAGCCCAGTTAGCAAGGTGCCGGTCACCCTGCAGGTTCCCAT  
AAAAACGATTGCAGCC

## **FIGURE 196**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56045
<subunit 1 of 1, 270 aa, 1 stop
<MW: 28317, pI: 6.00, NX(S/T): 1
MATGTRYAGKVVVVTGGGRGIGAGIVRAFVNNSGARVVICDKDESGGRALEQELPGAVFILCD
VTQEDDVKTIVSETIRRFGRILDGVNNAGHPPPQRPEETSAGQFRQLLELNLLGTYTLTKL
ALPYLRKSQGNVINISSLVGAIGQAQAVPYVATKGAVTAMTKALALDESPYGVRVNCISPGN
IWTPPLWEELAALMPDPRATIREGMLAQPLGRMGQPAEVGAAAVFLASEANFCTGIELLVTGG
AELGYGCKASRSTPVDAPDIPS
```

**Important features:**

**N-glycosylation site.**

amino acids 138-141

**Short-chain alcohol dehydrogenase family protein**

amino acids 10-22, 81-91, 134-171 and 176-185

## **FIGURE 197**

AGGCAGGGCAGCAGCTGCAGGCTGACCTTGCAGCTGGCGGAATGGACTGGCCTCACAAACCTG  
CTGTTTCTTCTTACCATTTCCATCTTCCTGGGCTGGGCCAGCCCAGGAGCCCCAAAAGCAA  
GAGGAAGGGCAAGGGCGGCCTGGCCCTGGCCCTGGCCCTCACAGGTGCCACTGGACC  
TGGTGTACGGATGAAACCGTATGCCCGCATGGAGGAGTATGAGAGGAACATCGAGGAGATG  
GTGGCCAGCTGAGGAACAGCTCAGAGCTGGCCAGAGAAAGTGTGAGGTCAACTTGCAGCT  
GTGGATGTCCAACAAGAGGAGCCTGTCTCCCTGGGCTACAGCATCAACCACGACCCCAGCC  
GTATCCCCGTGGACCTGCCGGAGGCACGGTGCTGTCTGGCTGTGAACCCCTTCACC  
ATGCAGGAGGACCGCAGCATGGTGAGCGTGCCCGTGTTCAGCCAGGTTCCGTGCCCGCCG  
CCTCTGCCGCCACCGCCCCGCACAGGGCCTGCCGCCAGCGCGAGTCATGGAGACCATCG  
CTGTGGCTGCACCTGCATCTTGAATCACCTGGCCAGAAGCCAGGCCAGCAGCCGAGA  
CCATCCTCCTTGCACCTTGCCAAGAAAGGCCTATGAAAAGTAAACACTGACTTTGAAA  
GCAAG

## **FIGURE 198**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59294
<subunit 1 of 1, 180 aa, 1 stop
<MW: 20437, pI: 9.58, NX(S/T): 1
MDWPHNLLFLLTISIFLGLGQPRSPKSKRKGQGRGPLAPGPHQVPLDLVSRMKPYARMEEY
ERNIEEMVAQLRNSSELAQRKCEVNLQLWMSNKRSLSPWGYSINHDPSRIPVVDLPEARCLCL
GCVNPFTMQEDRSMVSVPVFSQPVRRRLCPPPRTGPCRQRAVMETIAVGCTCIF
```

**Important features:**

**Signal peptide:**

amino acids 1-20

**N-glycosylation site.**

amino acids 75-78

**Homologous region to IL-17**

amino acids 96-180.

## **FIGURE 199**

GC GCCGCCAGCGTAGGC GG GGGTGGCCCTGCGTCTCCGCTTCCTGAAAAACCCGGCGGG  
CGAGCGAGGCTGCGGGCCGGCGCTGCCCTCCCCACACTCCCCGCGAGAACGCTCGCTCG  
GCGCCCAACATGGCGGGTGGCGCTGCCCGCAGCTAACGGCGCTCCTGGCCGCTGGAT  
CGCGCTGTGGCGCGACGGCAGGCCCGAGGAGGCCGCTGCCGCCGGAGCAGAGCCGGG  
TCCAGCCCAGACCCTCCAACGGACGCTGGTGTGGAGGGCGAGTGGAATGCTGAAATT  
TACGCCCATGGTGTCCATCCTGCCAGCAGACTGATTCAAATGGGAGGCTTGCAAAGAA  
TGGTGAATACTTCAGATCAGTGTGGGAAGGTAGATGTCATTCAAAGAACAGGTTGAGTG  
GCCGCTTCTTGTCAACCCTCCCAGCATTTCATGCAAAGGATGGGATATTCCGCCGT  
TATCGTGGCCCAGGAATCTTCAAGAACCTGCAGAATTATATCTTAGAGAAGAAATGGCAATC  
AGTCGAGCCTCTGACTGGCTGGAAATCCCCAGCTCTAACGATGTCTGGAATGGCTGGTC  
TTTTAGCATCTCTGGCAAGATATGGCATCTTCACAACATTTCACAGTGACTCTTGGAAATT  
CCTGCTTGGTGTCTTATGTGTGTTCTCGTCATGCCACCTTGGGTTTGGCCTTTATGGG  
TCTGGTCTTGGTGGTAATATCAGAATGTTCTATGTGCCACTTCCAAGGCATTATCTGAGC  
GTTCTGAGCAGAATCGGAGATCAGAGGAGGCTCATAGAGCTAACAGCTGAGGATGGGAG  
GAGGAAAAAGATGATTCAAATGAAGAAGAAAACAAGACAGCCTGTAGATGATGAAGAAGA  
GAAAGAAGATCTGGCGATGAGGATGAAGCAGAGGAAGAAGAGGAGGAGGACAACCTGGCTG  
CTGGTGTGGATGAGGAGAGAAGTGAGGCCATGATCAGGGGCCAGGAGAGGACGGTGTG  
ACCCGGGAGGAAGTAGAGCCTGAGGAGGCTGAAGAAGGCATCTGAGCAACCTGCCAGC  
TGACACAGAGGTGGAGAACACTCCTGAGGCAGCGTAAAGTCAGCATGCTGACAAGGGAC  
**TGTAGATTTAATGATGCGTTTCAAGAATACACACAAACATATGTCAGCTTCCCTTGG**  
CCTGCAGTTGTACCAAATCCTTAATTTCCTGAATGAGCAAGCTCTTAAAGATGCT  
CTCTAGTCATTGGTCTCATGGCAGTAAGCCTCATGTATACTAAGGAGAGTCTTCCAGGTGT  
GACAATCAGGATATAGAAAACAACGTAAGTGTGGATCTGTTGGAGACTGGGATGGGAA  
CAAGTTCATTTACTTAGGGTCAGAGAGTCTGACCAAGGAGGCCATTCCCAGTCATAATC  
AGCACCTTCAGAGACAAGGCTGCAGGCCCTGAAATGAAAGCCAAGCAGGAGCCTGGCT  
CCTGAGCATCCCCAAAGTGTAAAGCTAGAAGCCTGACATCCTTCTGTGAAAGTATTTAT  
TTTGTCAAATTGCAGGAAACATCAGGCACCACAGTCAGTGAAAAATCTTCACAGCTAGAA  
ATTGAAAGGGCTTGGGTATAGAGAGCAGCTCAGAAGTCATCCCAGCCCTGAAATCTCCTG  
TGCTATGTTTATTCTTACCTTAATTTCAGCATTCCACCATGGCATTCAAGGCTCT  
CCACACTCTCACTATTATCTCTGGTCAGAGGACTCCAATAACAGCCAGGTTACATGAAC  
TGTGTTGTCATTCTGACCTAACGGGTTAGATAATCAGTAACCATAACCCCTGAAGCTGT  
GACTGCCAACATCTCAAATGAAATGTTGTGGCCTCAGAGACTCAAAGGAAGTAAGGATT  
TTACAAGACAGATTAAGGAAACTGGTTGTCAGGAAAGTCTCTGAAAGTCTGCTGAAAGTGT  
AAGTTTCTAAGCAATATTTCAAGCCAGAAGTCCTCTAAGTCTGCTGAGTACAAGGTAGT  
CTTGTGAAGAAAAGTTGAATACTGTTTGTGTTCTCAAGGGGTTCCCTGGGTCTTGAAC  
TACTTAATAATAACTAAAAACCACTCTGATTTCCTCAGTGATGTGCTTTGGTGAAC  
GAATTAATGAACCTCCAGTACCTGAAAGTGAAGATTGATTGTTCCATCTCTGTAATC  
TTCCTAACAGAATTATATCTTGTAAATCTCTCAACTCAATCTACTGTAAGTACCCAGGGAG  
GCTAATTCTT

## **FIGURE 200**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56433
<subunit 1 of 1, 349 aa, 1 stop
<MW: 38952, pI: 4.34, NX(S/T): 1
MAGGRCGPQLTALLAAWIAAVAAATAGPEEAALPPEQSRVQPMTASNWTLMVEGEWMLKFYAP
WCPSCQQTDSEWEAFAKNGEILQISVGKVDVIQEPGLSGRFFVTTLPAFFHAKDGFRRYRG
PGIFEDLQNYILEKKWQSVEPLTGWKSPASLTMSGMAGLFSISGKIHHLHNYFTVTLGIPAW
CSYVFFVIATLVFGLFMGLVLVVISECFYVPLPRHLSERSEQNRSEEAHRAEQLQDAEEEK
DDSNEEENKDSLVDDEEEKEDLGDEDEAEEEEEDNLAAVGDEERSEANDQGPPGEDGVRE
EVEPEEAEEGISEQPCPADTEVVEDSLRQRKSQHADKGL
```

**Important features:**

**Signal peptide:**

amino acids 1-22

**Transmembrane domain:**

amino acids 191-211

**N-glycosylation site.**

amino acids 46-49

**Thioredoxin family proteins.** (homologous region to disulfide isomerase)

amino acids 56-72

**Flavodoxin proteins**

amino acids 173-187

## FIGURE 201

ATCTGGTTGAACTACTTAAGCTTAATTGTTAAACTCCGGTAAGTACCTAGCCCACATGATT  
TGACTCAGAGATTCTCTTTGTCCACAGACAGTCATCTCAGGGGCAGAAAGAAAAGAGCTCC  
CAAATGCTATATCTATTCAAGGGCTCTCAAGAACAAATGGAATATCATCCTGATTAGAAAAT  
TTGGATGAAGATGGATATACTCAATTACACTTCGACTCTCAAAGCAATACCAAGGATAGCTGT  
TGTTTCAGAGAAAGGATCGTGTGCTGCATCTCCTCCTGGCGCCTCATTGCTGTAATTGG  
GAATCCTATGCTTGGTAATACTGGTGATAGCTGTGGTCTGGGTACCATGGGGTTCTTCC  
AGCCCTTGTCTCCTAATTGGATTATATGAGAAGAGCTGTTATCTATTCAAGCATGTC  
AAATTCTGGATGGAAGTAAAAGACAATGCTGGCAACTGGGCTCTAATCTCCTAAAGATAG  
ACAGCTCAAATGAATTGGGATTATAGTAAAACAAGTGTCTTCCAACCTGATAATTCAATT  
TGGATAGGCCTTCTGGCCCCAGACTGAGGTACCATGGCTCTGGGAGGATGGATCAACATT  
CTCTCTAACTTATTTCAGATCAGAACACAGCTACCCAAAGAAAACCCATCTCCAATTGTG  
TATGGATTACGTGTCAGTCATTATGACCAACTGTGTAGTGTGCCCTCATAGTATTG  
GAGAAGAAGTTTCAATGAAGGAAGGGTGAGAAGGAGAGAATATGTGAGGTAGTA  
AGGAGGACAGAAAACAGAACAGAAAAGAGTAACAGCTGAGGTCAAGATAATGCAGAAAATG  
TTTAGAGAGCTGGCCAAGTGTAACTCTAACCAAGAAATTGAAGGGAGAGGCTGTGATTCT  
GTATTGTCGACCTACAGGTAGGCTAGTATTATTTCTAGTTAGTAGATCCCTAGACATGG  
AATCAGGGCAGCCAAGCTTGAGTTTATTATTTATTATTTGAGATAGGGTCT  
CACTTGTACCCAGGCTGGAGTGCAGTGGCACAACTCGACTCACTGCAGCTATCTCGC  
CTCAGCCCCCTCAAGTAGCTGGACTACAGGTGCATGCCACCAGGCTAATTTGGTG  
TTTTTGAGAGACTGGTTTGCCATGTTGACCAAGCTGGCTCTAACTCCTGGCTTAAG  
TGATCTGCCCGCTGGCTCCAAAGTGCTGGATTACAGATGTGAGCCACCACACCTGGC  
CCCAAGCTTGAATTTCATTGCCCCCTGCTTACAGTTGACTGGCATTCCTGGTAAGGCCATAAGCGA  
ATCTTAATTCTGGCTCTATCAGAGTTGTTCATGCTCAACAATGCCATTGAAGTGCACGGT  
GTGTTGCCACGATTGACCTCAACTCTAGCAGTATCAGTTATGAACTGAGGGTGAAT  
ATATTCTGAATAGCTAAATGAAGAAATGGAAAAAAATCTTCACCACAGTCAGAGCAATT  
ATTATTTCTCATCAGTATGATCATAATTATGATTATCATCTTAGTAAAAGCAGGAACCTCTA  
CTTTTCTTATCAATTAAATAGCTCAGAGACTACATGCCATTCTCTAAATAGAATCTT  
TTTTTTTTTTTTGAGACAGAGTTCGCTTTGTCCTGGCAGGCTGGAGTGCACGG  
CACGATCTCGGCTACCGCAACCTCCGCCCCCTGGGTTCAAGCAATTCTCTGCCTCAGCCT  
CCCAAGTAGCTGGATTACAGTCAGGCCACCACACCCGGCTAATTTGTATTGTTAGT  
AGAGACAGGGTTCTCCATGTCGGTCAGGTAGTCCGAACCTCTGACCTCAAGTGTACTGC  
CTGCCTCGGCCTCCAAAGTGTGGATTACAGGCGTGAGCCACTGCACCCAGCCTAGAATCT  
TGTATAATATGTAATTGTAGGGAAACTGCTCTAGGAAAGTTTCTGCTTTAAATACA  
AAAATACATAAAATACATAAAATCTGATGATGAATATAAAAAGTAACCAACCTCATTGGA  
ACAAGTATTAACATTGGAAATATGTTTATTAGTTGATGTACTGTTACAATT  
ACCATTGTTTCAGTAATTACTGTAAAATGGTATTATTGGAATGAAACTATATTCTCATG  
TGCTGATTGTCCTATTCTCATCTTCCACTGGTGCTATTGTTATTCCAAATGGATA  
TTCTGTATTACTAGGGAGGCATTACAGTCCTCTAATGTTGATTAATATGTGAAAAGAAAT  
TGTACCAATTACTAAATTATGCAGTTAAAATGGATGATTGTTATGTTATGTGGATT  
TTCAATAAAAAAAAAACTCTTATCAAAAAAAAAAAAAAA

## FIGURE 202

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53912
<subunit 1 of 1, 201 aa, 1 stop
<MW: 22563, pI: 4.87, NX(S/T): 1
MEYHPDLENLDEDGYTQLHFDSQSNTRIAVVSEKGSCAASPPWRLIAVILGILCLVILVIAV
VLGTMGVLSLSSPCPPNWIYEKSCYLFMSMSLNWDGSKRQCWLGSNLLKIDSSNELGFIVKQ
VSSQPDNSFWIGLSRPQTEVPWLWEDGSTFSSNLFQIRTTATQENPSPNCVWIHVSVIYDQL
CSVPSYSICEKKFSM
```

**Important features:**

**Type II transmembrane domain:**

amino acids 45-65

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 197-200

**N-myristoylation sites.**

amino acids 35-40 and 151-156

**Homologous region to LDL receptor**

amino acids 34-67 and 70-200.

## **FIGURE 203**

GGAGGGGAGGAGCAGGCCACACAGGCACAGGCCGGTGAGGGACCTGGAGGGTCTCGCTCTGTCA  
CACAGGCTGGAGTGCAGTGGTGTGATCTTGGCTCATCGTAACCTCCACCTCCGGGTTCAAGTGATTCTCATGCC  
TCAGCCTCCCAGTAGCTGGATTACAGGTGGTACTTCCAAGAGTGACTCCGTCGGAGGAAATGACTCCAG  
TCGCTGTCAGACACTGTTCTGCTGAGTCTGCTCTGGCCAAGGTGCCACGGCAGGGGCCACAGG  
GAAGACTTCGCTTCTGAGCCAGCGAACAGACACACAGGAGCAGCCTCACTACAAACCCACACCAGACCTG  
CGCATCTCATCGAGAACTCCGAAGAGGCCCTCACAGTCATGCCCTTCCCTGAGGCCACCCCTGCTTCCCGA  
TCCTCCCTGACCCAGGGGCTTACCACTTCTGCTCTACTGGAACCGACATGCTGGAGATTACATCTTC  
TATGGCAAGCGTACTTCTGCTGAGTGACAAAGCCTTAGCCTCTGCTTCCAGCACCAAGGAGGAGCCTG  
GCTCAGGGCCCCCGCTTAGCCACTTCTGTCACCTCTGGAGGCCCTCAGAACATCAGCCTGCCAGTGCC  
GCCAGCTTACCTTCTCCACAGTCCTCCACAGGCCGCTCACAATGCTCGGTGACATGTGCGAGCTC  
AAAAGGGACCTCCAGCTGCTCAGCCAGTTCTGAAGCATTCCAGAAGGCCCTCAAGGAGGCCCTGGCTGCC  
GCCAGCCAGCAGTTGAGGCCCTGAGTCGAAACTGACCTCTGAGATTATGGGGACATGGTGTCTTCGAG  
GAGGACCGGATCAACGCCACGGTGGAAGCTCCAGGCCACAGCCGCCCTCAGGGACCTGACATCCACTCCGG  
CAGGAGGAGGAGCAGAGCGAGATCATGGAGTACTCGGTGCTGCTCGAACACTCTTCAGAGGAGCAAAGGC  
CGGAGCGGGGAGGCTGAGAAGAGACTCCTCTGGTGGACTTCAGCAGCCAAGGCCCTGTTCCAGGACAAGAATTCC  
AGCCAAGTCTGGGTGAGAAGGTCTGGGATGTGGTACAGAACACCAAAGTAGCCAACCTCACGGAGGCCGTG  
GTGCTCACTTCCAGCACCAGTACAGCGAAGAATGTGACTCTGCAATGTGTTCTGGTGAAGAACCCCCACA  
TTGAGCAGCCCGGGCATTGGAGCAGTGTGCTGGTGGAGACCGTCAGGAGAGAACCCAAACATCCTGCTTCTGC  
AACCACTTGACCTACTTGCACTGCTGATGGTCTCCTCGGTGGAGGTGGACGCCGTGACAAGCACTACCTGAGC  
CTCCTCTCTACGTGGGTGTGCTCTGCCCTGCCCTGCTGCACTTGTGACCATTCGCGCTTACCTCTGCTTCCAGG  
GTGCCCTCGCCGTGCAAGGAGAACCTCGGGACTACACCATCAAGGTGCAATGAACCTGCTGCTGGCGAGCAGTGC  
CTGCTGGACACGAGCTTCTGCTCAGCGAGCCGGTGGCCCTGACAGGCTCTGAGGCTGGCTGCCAGGAGTGC  
ATCTTCTGCACTTCTCCCTGCTCACCTGCCCTTCTGGATGGGCTCGAGGGTACACCTCTACCGACTCGTG  
GTGGAGGTCTTGGCACCTATGTCCCTGGCTACCTACTCAAGCTGAGGCCATGGGCTGGGCTTCCCATCTT  
CTGGTACGCTGGTGGCCCTGGTGGATGTGGACAACATGGCCCATCATCTGGCTGTGCAAGGACTCCAGAG  
GGCGTCATCTACCCCTCATGTGCTGGATCCGGGACTCCCTGGTCAGCTACATACCAACCTGGCCTTCTCAGC  
CTGGTGTCTGTTCAACATGGCCATGCTAGCCACCATGGTGGTGCAGATCCTGCGGCTGCCCTGGCCTTGATCTTCTCC  
AAGTGGTACATGTGCTGACACTGCTGGGCTCAGCCTGGCTTGGCCCTGGGCTTGGGCTTGGGCTTCCATCTT  
TTGCTTCTGGCACCTTCAGCTTGTGCTCTACCTTTCAGCATCATCACCTCTTCCAAGGCTTCTCATC  
TTCATCTGGTACTGGCATGCGGTGCAGGCCGGGGTGGCCCTCCCTCTGAAGAGCAACTCAGACAGCGCC  
AGGCTCCCATCAGCTCGGGCAGCACCTCGTCAGCCGATCTAGGCCCTCAGGCCACCTGCCATGTGATGAAG  
CAGAGATGCGCCTGTCGCACACTGCTGTGGCCCCGAGCCAGGCCAGGCCAGGCCAGTGCAGCCGAGACT  
TTGAAAGCCAACGACCATGGAGAGATGGGCCATGGTGGACGGACTCCGGGCTGGGCTTTGAATTG  
GCCTGGGACTACTCGGCTCTCACTCAGCTCCACGGGACTCAGAAGTGCGCCGCACTGTCAGCTAGGGTACTG  
TCCCACATCTGCCCACCCAGCTGGAGGCCCTGGTCTCTCCTTACACCCCTGGGCCAGGCCCTCATTGCTGG  
GGCAGGCCCTGGATCTTGAGGGCTGGCACATCCTTAATCCTGTGCCCTGCTGGACAGAAATGTGGCTCCA  
GTTGCTCTGCTCTCGTGGTACCCCTGGGACTCTGCACTCTGCTGATCTCTGTCAATTAACTCAGGTGGCACCCAGGG  
CGAATGGGGCCAGGGCAGACCTTCAGGGGAGGCCCTGGGGAGAGGCCCTTGTGCAAGGAGCACCCAGGG  
AGCTCGCCTACCTCTGAGGCCAGGCCCTCCCTCAGCCCCCAGTCCTCCCTCCATCTTCCCTGGGTT  
TCCCTCTCCAGGCCCTGGTCTCTGCTCTGTTACAGCTGGGGCTCCCTGCAAGGCTCTGAGGCCCTGGG  
GTGGTTCCAGGAGCTGCTGGTCTGGCTAGGTCCCTCTGCACTCTGAGGCCCTGGTGTATGAGCTGCAATTGCC  
GGCTGGTACCGATGCGTGGCTGGCTAGGTCCCTCTGCAAGGCTCTGAGGCCCTGGTGTAGGTGGCAAGA  
CTGCAAGGCCCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGG  
CTCACCTGACCAAGCACGCCCTAGAGGGGCCCTGCCCTGCAAGGCCCTGGTGTAGGTGGCAAGA  
CCATGCCAGTCCCGTCTGGTTCCATCCCACCACTCCAAGGACTGAGACTGACCTCTCTGGTGACACTGCC  
GAGCCTGACACTCTCTAAGAGGTCTCTCCAAGGCCCAAATAGCTCCAGGCCCTGCCGCCATCATGGT  
TAATTCTGTCACAAACACACAGGGTAGATTGCTGGCCTGTTGAGGTGGTAGGGACACAGATGACCGACCTG  
GTCACTCCTCTGCCAACATTAGCTGGTATGTGAGGGCTGCGTGAGCAAGAACCTGGAGCTACAGGGACA  
GGGAGGCCATCTCTGCCGGGATCCTGGAGACTCCTGCAAGGAGTCAGCGTTCAATTGACCTTGAGAG  
GGGAAGGATGTTCTTTACGTACCAATTCTTGTCTTGTATATAAAAAGAAGTACATGTTCAATTGTAGAGA  
ATTGGAAACTGTAGAAGAGAATCAAGAAGAAAATAAAAAATCAGCTGTTGTAATCGCCTAGCAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAA

## FIGURE 204

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50921
<subunit 1 of 1, 693 aa, 1 stop
<MW: 77738, pI: 8.87, NX(S/T): 7
MTPQSLLQTTLFLLSLLFLVQGAHGRGHREDFRFCSQRNQTHRSSLHYKPTPDLRISIENSE
EALTVHAPFPAAHPASRSFPDPRGLYHFCLYWNRHAGRLHLLYGRDFLLSDKASSLLCFQH
QEESLAQGPPPLLATSVTSPWSPQNISLPSAASFSTFSFHSPPHTAAHNASVDMCELKRDQLL
SQFLKHPQKASRRPSAAPASQQLQSLQESKLTSVRFMGDMVSFEEDRINATVWKLQPTAGLQD
LHIHSRQEQQSEIMEYSVLLPRTLQRTKGRSGAEKRLLLVDFSSQALFQDKNSSQVLGE
KVLGIVVQNTKVANLTEPVVLTQHQQLQPKNVTLQCVFWEDPTLSSPGHWSSAGCETVRRE
TQTSCFCNHLYFAVLMVSSVEVDAVHKHYLSLLSYVGCVVSALACLVTIAAYLCSRVPLPC
RRKPRDYTIKVHMNLLAVFLLDTSFLLSEPVALTGSEAGCRASAIFLHFSLTCLSWMGLE
GYNLYRLVVEVFGTYVPGYLLKLSAMGWGFPIFLVTIVALVDVDNYGPIILAVHRTPEGVIY
PSMCWIRDSLVSYITNLGLFSLVFLFNMAMLATMVVQILRLRPHTQKWSHVLLGLSLVLG
LPWALIFFSFASGTQQLVVLYLFSIITSFQGFLIFIWYWSMRLQARGGPSPLKSNSDSARLP
ISSGSTSSSRI
```

**Important features:**

**Signal peptide:**

amino acids 1-25

**Putative transmembrane domains:**

amino acids 382-398, 402-420, 445-468, 473-491, 519-537, 568-590  
and 634-657

**Microbodies C-terminal targeting signal.**

amino acids 691-693

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 198-201 and 370-373

**N-glycosylation sites.**

amino acids 39-42, 148-151, 171-174, 234-237, 303-306, 324-327  
and 341-344

**G-protein coupled receptors family 2 proteins**

amino acids 475-504

## **FIGURE 205**

TGCCTGGCTGCCTGTCAACAATGCCGTTACTCTGCTTCCAGGTTGCCCTGCCTGCAGA  
GGAAANCNTCGGGACTACACCNTCAAGTGCACATGAACCTGCTGCTGGCCGTCTCCTGCTG  
GACACGAGCTTCCTGCTCAGCGNAGCCGGTGGCCCTGACAGGCTCTGAAGGCTGGCTGCCGA  
GCCAGTGCCATCTTCCTGCACCTCTCCTGCTCACCTGCCTTCCTGGATGGCCTCGAGGGG  
TACAACCTCTACCGACTCGTGGTGGAGGTCTTGGCACCTATGTCCCTGGCTACCTACTCAA  
GCTGAGCGCCATGGGCTGGGCTTCCCCATCTTCTGGTGACGCTGGTGGCCTGGTGGATG  
TGGACAACTATGGCCCCATCATCTTGGCTGTGCATAGGACTCCAGAGGGCGTCATCTACCCT  
TCCATGTGCTGGATCCGGACTCCCTGGTCAGCTACATCACCAACCTGGCCTTTCAGCCT  
GGTGTTCCTGTTAACATGG

**FIGURE 206**

CGGACGCGTGGGCCGACGCGTGGGCCGACGCGTGGGCCGACGCGTGGCTGGTTAGGAAAAAGTTGGATGGGATTATGTGAAACTACCCCT  
TCCTTTCAAAAATGGAGACACAGAAGAGGGCTCTAGGAAAAAGTTGGATGGGATTATGTGAAACTACCCCT  
GCGATTCTCTGCTGCCAGAGCAGGCTGGCGCTCCACCCCCAGTGCAGCCTCCCTGGCGGGTGGTAAAGAGAC  
TCGGGAGTCGCTGCTCCAAAGTGCCCCCGCTGAGTGAAGCTCAGCCCAGTCAGCAAATGGACCTCTCGGGC  
TTCTCCTGCTGACATCTGCCCTGGCGGCCAGAGACAGGGACTCAGGCCAATCAAACCTGAGTAGTAAATTCC  
AGTTTCCAGCAACAAGGAACAGAACGGAGTACAAGATCCTCAGCATGAGAGAATTATTACTGTGCTACTAATG  
GAAGTATTACAGCCCAAGGTTCCCTACACTTATCCAAGAAATACGGTCTGGATGGAGATTAGTAGCAGTAG  
AGGAAAATGTATGGATACAACCTACGTTGATGAAAGATTGGGCTTGAAGACCCAGAAGATGACATATGCAAGT  
ATGATTGTAGAAGTTGAGGAACCCAGTGATGGAACATATAATTAGGGCCTGGTGGTCTGGTACTGTACCG  
GAAAACAGATTCTAAAGGAATCAAATTAGGATAAGATTGTATCTGATGAAATATTTCCTCTGAACCAGGGT  
TCTGCATCCACTACACATTGTCATGCCACAATTACAGAACGGTGTGAGTCCTCAGTGCACCCCCCTCAGCTT  
TGCCACTGGACCTGCTTAATAATGCTATAACTGCCCTTAGTACCTTGGAGAGACCTTATTGATATCTGAAACAG  
AGAGATGGCAGTTGGACTTAAAGATCTATAAGGCCAACCTTGGCAACTCTTGGCAAGGTTTGTGTTTGGAA  
GAAAATCCAGAGTGGTGGATCTGAACTTCTAAACAGAGGGAGGTAAGATTATAACAGTCACACCTGTAACCTCT  
CAGTGTCCATAAAGGAAGAACCTAAAGAGAACCGATACCATTCTGCCAGGGTGTCTCTGGTTAACAGCTGTG  
TGDDGAACACTGTGCCCTGTTGTCCTCCAAATTGCAATGTAATGTCAATGTGCTTCAAGGAAAGTTACTAAAAAATACC  
ACGAGGTCTTCAGTTGAGACCAAAAGACGGTGTCAAGGGATTGCACAAATCACTCACCGACGTGGCCCTGGAGC  
ACCATGAGGAGTGTGACTGTGTCAGAGGGAGCACAGGAGGTAGCCGCATCACCAACAGCAGCTCTGCCCA  
GAGCTGTGAGTGCAGTGGCTGATTCTATTAGAGAACGTATGCGTTATCCATCTTAACTCAGTTGTTGCT  
TCAAGGACCTTCATCTCAGGATTACAGTGCATCTGAAAGAGGAGACATCAAACAGAATTAGGAGTTGCGA  
ACAGCTCTTGAGAGGAGGCCAAAGGACAGGAGAAAAGGCTTCAATGTTGAAAGAAAATTAAATGTTGAT  
TAAATAGATCACCAAGCTAGTTCAGAGTTACCATGTAAGTATTCCACTAGCTGGGTTCTGTATTTCAGTTCTTC  
GATACGGCTAGGGTAATGTCAGTACAGGAAAAAAACTGTGCAAGTGAGCACCTGATTCCGTTGCTTAAAC  
TCTAAAGCTCCATGTCCTGGCCTAAATGTTAAATCTGGATTTTTTTTTTGCTCATATTACAT  
ATGTAACCAAGAACATTCTATGTAACAAACCTGGTTTAAAAGGAACATGTTGCTATGAAATTAAACTGT  
GTCATGCTGATAGGACAGACTGGATTTCATATTCTTATTAAAATTCTGCCATTAGAAGAGAACACTACA  
TTCATGGTTGGAAAGAGATAAACCTGAAAAGAACAGTGGCCTTATCTTACATTGACATTATAACTGTTGCTTTCT  
TTTCATTGTCACATTTTATATTCTCTTTGACATTATAACTGTTGCTTTCTAATCTTGTAAATTATATCT  
ATTTTACCAAAGGTATTAAATTCTTTTATGACAACCTAGATCAACATTNTTGTGTTAAATTCT  
AAACACAAATTGTTAGCCAGAGGAACAAAGATGATAAAATATTGTTGCTCTGACAAAAAATACATGTTATTCA  
TTCTCGTATGGCTAGAGTTAGATTAACTGCAATTAAAAACTGAATTGGAAATAGAATTGTTGAAAGTGTGAAA  
GACTTTGGAAAAATTAAATTATCATCTTCCATTCTGTTATTGGAGGATGAAAATAAAAGAACACTATG  
AAAGTAGACATTGAGTCAGCAGGCAATTACTAACCTATTCTCTTTGGGGAAATCTGAGCCTAGCTCAGAAAAACAT  
AAAGCACCTGGAAAAAGACTGGCAGCTCTCTGATAAAGCGTGTGCTGAGTAGGAACACATCCTATT  
TTGTGATGTTGTTGTTTATTCTTAAACTCTGTTCCATACACTGTATAAATACATGGATATTGTTATGTACA  
GAAGATGTCCTTAACCAGGTCAGTTATTGTAACCTGCAATTAAAAGAAAATCAGTAAAATATTGTTATGTACA  
AAAATGCTTAATATNGTCCTAGGTTATGTGGTGAACATTGAAATCAAAATGTATGAAATCATCAAATAAAAGA  
ATGTCGCTATTGGGAGAAAATTAAAAAAAGGTTAGGGATAACAGGGTAATGCGGCC

## **FIGURE 207**

MSLFGLLLTSLAGQRQGTQAESNLSSKFQFSSNKEQNGVQDPQHERIITVSTNGSIHS  
FPHTYPRNTVLVWRLVAVEENVWIQLTFDERFGLEDPEDDICKYDFVEVEEP  
SDGTILGRWC  
GSGTVPKGKQISKGNQIRIFVSDEYFPSEPGFCIHYNIVMPQFTEAVSPSVLPPS  
ALPLDLL  
NNAITAFSTLEDLIRYLEPERWQLDLEDLYRPTWQLLGKA  
FVFGRKS  
RVVDLNLLTEEVRLY  
SCTPRNF  
SVSIREELKRTDTIFWP  
GCLLVKRCGGNCACCLHNCNECQC  
CVPSKVTKKYHEV  
LRPKTGVRGLHKSLTDVALEHHEECDCVCRGSTGG

**Signal sequence:**

amino acids 1-14

## FIGURE 208

CCCATCTCAAGCTGATCTGGCACCTCTCATGCTCTGCTCTCAACCAGACCTTACATCCATTGGAAAGA  
AGACTAAAAAATGGTGTCCAATGTGGACACTGAAGAGACAAATTCTTACCTTTAACATAATCCTAATTTC  
AAACTCCTGGGCTAGATGGTTCTAAAACCTGCCCCGTGATGTCACTCTGGATGTTCAAAGAACCATGTG  
ATCGTGGACTGCACAGACAAGCATTTGACAGAAATTCTGGAGGTATTCCCACCGAACACCAGAACCTCACCC  
ACCATTAACCACATACCAAGACATCTCCCCAGCAGTCTTACAGACTGGACATCTGGTAGAGATCGATTTCAGA  
TGCAACTGTGTACCTATTCCACTGGGGTCAAAAACACATGTGATCAAGAGGCTGCAGATTAAACCCAGAAC  
TTTAGTGGACTCACTTATTAAAATCCCTTACCTGGATGGAACCAAGAGCTACTAGAGATACCGCAGGGCTCCCG  
CCTAGCTTACAGCTCTAGCCTTGAGGCCAACACATCTTCCATCAGAAAAGAGAACTTAACAGAACACTGGCC  
AACATAGAAATACTCTACCTGGCAAAAGTGTATTATCGAAATCTTGTATGTTCATATTCAATAGAGAAA  
GATGCCCTCTAAACTTGACAAAGTAAAAGTGTCTCCCTGAAAGATAACAATGTACAGCCGTCCACTGTT  
TTGCCATCTACTTAACAGAACTATATCTTACAACAACATGATTGCAAAAATCCAAGAAGATGATTAAATAAC  
CTCAACCAATTACAAATTCTTGACCTAAGTGGAAATTGCCCTCGTTATAATGCCCATTTCTTGCGCCG  
TGAAAAATAATTCTCCCTACAGATCCCTGAAATGCTTTGATGCCGTGACAGAAATTAAAGTGTCTACGTCTA  
CACAGTAACCTCTTCAGCATGTGCCCAAGATGGTTAAAGAACATCAACAAACTCCAGGAACGGATCTGTCC  
CAAAACTCTGGCCAAGAAATTGGGATGCTAAATTCTGCATTCTCCAGCCTCATCCAATTGGATCTG  
TCTTCAATTGAACTCAGGTCTATCGTGCATCTATGAATCTATCACAAGCATTCTCACTGAAAAGCCTG  
AAAATTCTGGGATCAGAGGATATGCTTAAAGAGCTTAAACCTCTGCCATTACATAATCTTCAA  
AACTCTGAAAGTTCTTGATCTTGCACTAACTTATAAAAATTGCTAACCTCAGCATGTTAAACAATTAAAAGA  
CTGAAAGTCATAGATCTTCAGTGAAATAAATCACCTCAGGAGATTCAAGTGAAGTGGCTTCTGCTCAAAT  
GCCAGAACTCTGTAGAAAGTTATGAACCCAGGTCTGGAAACAATTACATTATTTCAGATATGATAAGTATGCA  
AGGAGTTGCAAGATTCAAAACAAAGAGGCTTCTTCATGCTGTTAATGAAAGCTGCTACAAGTATGGCAGACC  
TTGGATCTAAGTAAAATAGTATTTTGTCAGTCCTCTGATTTCAGCATCTTCTTCAATGCTCAAATGCCCTG  
AACTCTGTCAGGAAATCTCATTAGCCTAACCTCTTCAATGGCAGTGAATTCCAACCTTCTGAGAGCTGAGATATTG  
GACTTCTCCAACAACCGCTGATTACTCCATTCAACAGCATTGAAAGAGCTTACAAACTGGAAGTCTGGAT  
ATAAGCAGTAAAGCATTATTTCAATCAGAAGGAATTACTCATATGCTAAACTTACCAAGAACCTAAAGGTT  
CTGCAGAAACTGATGATGAACGACAATGACATCTTCTCCACAGCAGGACCATGGAGAGTGAGTCTTCTAGA  
ACTCTGGAATTCAAGAGGAATTAGACATCTCTAAAATTCCCTAAGTTCTGCCCTCTGGAGTTTGATGGT  
ATGCCTCAAATCTAAAGAATCTCTTGGCCAAAATGGCTCAAATCTTCTGTTGAGAAACTCCAGTGT  
CTAAAGAACCTGGAAACTTGGACCTCAGCCACAACCAACTGACCACTGTCCTGAGAGATTATCCAACCTGTTCC  
AGAACCTCAAGAATCTGATTCTTAAAGATAATCAAATCAGGAGTCTGACGAAGTATTCTACAAGATGCCCTC  
CAGTTGCGATATCTGGATCTCAGCTCAAATAAATCCAGATGATCCAAAGACAGCTTCCAGAAAATGCTCCTC  
AACATCTGAAGATGTTGCTTTGATCATAATGGTTCTGTGCACCTGTGATGCTGTGTTGCTGGTGG  
GTAAACCATAAGGAGGTGACTATTCTTACCTGGCACAGATGTGACTTGTGAGGGCCAGGAGCACACAAGGGC  
CAAAGTGTGATCTCTGGATCTGATCACCTGTGAGTTAGATCTGACTAACCTGATTCTGTTCTCACTTTCCATA  
TCTGTATCTCTTCTCATGGTGTGATGAGCAGCAGCTAACCTCTATTCTGGGATGTGTTGATATTACCAT  
TTCTGTAAGGCCAAGATAAAAGGGTATCAGCGTCTAAATCACAGACTGTTGCTATGATGCTTTATGTGAT  
GACACTAAAGACCCAGCTGTGACCGAGTGGTTTTGGCTGAGCTGGCCAAACTGGAAGACCCAAAGAGAGAAA  
CATTTAAATTATGTCAGGAAAGGACTGGTTACAGGGCAGCAGTTCTGGAAAACCTTCCAGAGCATA  
CAGCTTAGCAAAAGACAGTGTGTTGATGACAGACAAGTATGCAAAGACTGAAAATTAAAGATAGCATTTCAC  
TTGTCCTCATCAGAGGCTATGGATGAAAAAGTGTGATTATCTGATATTCTTGAGAAGGCCCTTCAGAAG  
TCCAAGTCTCCAGCTCCGGAAAAGGCTCTGTGGGAGTCTGTGCTTGTGAGTGGCCAACAAACCCGCAAGCTCAC  
CCATACTCTGGCAGTGTCTAAAGAACGCCCTGGCCACAGACAATCATGTGGCTATAGTCAGGTGTTCAAGGAA  
ACGGTCTAGCCTTCTTGCAAAACACAACGTCTAGTTACCAAGGAGAGGCCGGC

## FIGURE 209

MVFPMWTLKRQILILFNIILISKLLGARWFPTLPCDVTLDPKHNHIVDCTDKHLTEIPGG  
IPTNTTNLTLTINHIPDISPASFHRLDHLVEIDFRCNCVPIPLGSKNNMCIKRLQIKPRSFS  
GLTYLKSLYLDGNQNLLEIPQGLPPSLQLLSLEANNIFSIRKENTELANIEILYLGQNCYR  
NPCYVSYSIEKDAFLNLTKLKVLSLKDNNTAVPTVLPTSTELYLYNNMIAKIQEEDDFNNL  
NQLQILDLSGNCPRCYNAPFFCAPCKNNSPLOIPVNNAFDALTELKVRLHSNSLQHVPPRWF  
KNINKLQELDLSQNFNLAKEIGDAKFLHFLPSLIQLDLSFNFELQVYRASMNLSQLAFSSLKSL  
KILRIRGYVFKELKSFNLSPLHNLQNLLEVLDLGTNFIFKIANLSMFQFKRLKVIDLSVNKIS  
PSGDSSEVGFCASNARTSVESYEPOVLEQLHYFRYDKYARSCRFKNKEASFMSVNESCYKYGQ  
TLDLSKNSIFFVKSSDFQHLSFLKCLNLSGNLISQTLNGSEFQPLAELRYLDFSNNRLDLLH  
STAFAEELHKLEVLDISSIONSHYFQSEGITHMLNFTKNLKVLQKLMMNNDNISSTSRTMESES  
LRTLEFRGNHLDVLWREGDNRYLQLFKNLLKLEELDISKNSLSFLPSGVFDGMPPNLKNL  
AKNGLKSFSWKKLQCLKNLETLDLSHNQLTTVPERLSNCSRSKLNLLKNNQIRSLTKYFLQ  
DAFQLRYLDLSSNKIQMIQKTSFPENVNNLKMLLHHNRFLCTCDAVWFVWWVNHTEV  
YIYHFCKAKIKGYQRLISPDCCYDAFIYDTPKDPAVTEWVLAELVAKLEDPREKHFNL  
RDWLPGPVLENLSQSIQLSKKTVFVMTDKYAKTENFKIAFYLSHQRLMDEKVDV  
KPFQSKFLQLRKRLCGSSVLEWPTNPQAHPYFWQCLKNALATDNHV  
AYSQVFKETV

**Signal sequence:**

amino acids 1-26

**Transmembrane domain:**

amino acids 840-860

## **FIGURE 210**

GGGTACCATTCTCGCCTGCTGCAAGTTACGGAATGAAAAATTAGAACAAACAGAAACATGGAAAACATGTTCCCTTC  
AGTCGTCAATGCTGACCTGCATTTCCTGCTAATATCTGGTCTGTGAGTTATGCGCCGAAGAAAATTTCATA  
GAAGCTATCCTGTGATGAGAAAAGCAAATGACTCAGTTATTGCGAGGTGCAGCAATCGACTACAGGAAG  
TTCCCCAAACGGTGGGCAAATATGTGACAGAACTAGACCTGTCTGATAATTTCATCACACACATAACGAATGAAT  
CATTCAGGGCTGCAAATCTCACTAAAATAATCTAAACCACAACCCCAATGTACAGCACCAGAACGGAAATC  
CCGGTATAACAATCAAATGGCTTGAATATCACAGACGGGCATTCTCAACCTAAAAACCTAAGGGAGTTACTGC  
TTGAAGACAACCAGTTACCCAAATACCCCTGGTTGCCAGAGTCTTGACAGAACTTAGTCTAATTCAAACAA  
ATATATAACAACATAACTAAAGAGGGCATTCAAGACTTATAAAACTCTGAAAAACTCTATTGGCTGGAACGT  
ATTITAACAAAGTTGCGAGAAAACAATAGAACATAGAAGATGGAGTATTGAAACGCTGACAAATTGGAGTTGCTAT  
CACTATCTTCAATTCTCTTACACGTGCCACCCAAACTGCCAAGCTCCCTACGCAAACCTTTCTGAGCAACA  
CCCAGATCAAATACATTAGTGAAGAAGATTCAAGGGATTGATAAATTAAACATTACTAGATTAAAGGGGAAC  
GTCGGAGGTGCTTCAATGCCCAATTCCATGCGTGCCTGTGATGGGGTGTCAATTAAATAGATGTTTGG  
CTTTCAAAACTGACCCAACTTCGATACTAAACCTCTAGCACTCCCTAGGAAGATAATGCTGCCCTGG  
TTAAAAATATGCTCATCTGAAGGTGCTGGATTTGAACTATTAGTGGAGAAATAGTCTCTGGGGCAT  
TTTAACGATGCTGCCCGCTTAGAAATACTGACTTGTCTTTAACTATATAAAGGGAGTTATCCACAGCATA  
TTAATATTCCAGAAACTCTCTAAACTTTGTCTTACGGGCAATTGCAATTAAAGGGTTATGTGTTCAAGGAAC  
TCAGAGAAGATGATTCCAGCCCTGATGCAGCTCCAACTTATGACTATCAACTTGGGTATTAATTAA  
AGCAAACTGATTCAAACCTTTCCAAAATTCTCCAATCTGAAATTATTTACTTGTCAAGAAAACAGAAATATCAC  
CGTTGGAAAAGATACCCGGAGAGTTATGCAAATAGTCTCTTCAACGTATATCCGAAACGACGCTCAA  
CAGATTGAGTTGACCCACATTGAACTTTATCATTTCACCCGCTTTAAATAAAGCCACAATGTGCTGCTT  
ATGGAAAAGCCCTAGATTAAAGCTAACAGTATTCTTCAATTGGGCAAACCAATTGAAAATCTTCTGACA  
TTGCTGTTAAATCTGCTGCAAATAGCAATGCTCAAGTGTAAAGTGGAACTGAAATTTCAGCCATTCTCATG  
TCAAATATTGAGATTGACAAACAAATAGACTAGACTTGTGAAATGCTAGTGTCTTACTGAAATTGTCCGACTTGG  
AAGTCTAGATCTCAGCTATAATTCAACTATTCAAGAACATAGCAGGGTAACACATCATCTAGAAATTATTCAA  
ATTTCACAAATCTAAAGTTTAAACTTGAGCCACAACACATTATCTTAAACAGATAAGTATAACCTGGAAA  
GCAAGTCCCTGGTAGAATTAGTTTCAGTGGCAATGCCCTGACATTGTGAAATGATGACAAACAGGTATA  
TCTCCATTTCAAAGGTCTCAAGAACATGACACCGTCTGGATTATCCTTAATAGGCTGAAAGCACATCCAAATG  
AAGCATTCCATTTCAGCAGCTCACTGAACATACATATAATGATAATATGTTAAAGTTTAACTGG  
CATTACTCCAGCAGTTCTCGTCTGAGTTGACTTACGTGGAAACAAACTACTCTTTAACTGATGAGCC  
TATCTGACTTACATCTCCCTCGACACTGCTGAGTCATAACAGGATTCCACCTACCCCTGGCTTCT  
TTTCTGAAGTCAGTAGTCTGAAGCACCTCGATTAAAGTCCAATCTGCTAAAACAATCAACAAATCCGACTTG  
AAACTAAGACCACCACAAATTATCTATGTTGAAACTACAGGAAACCCCTTGAAATGACCTGTGACATTGGAG  
ATTTCGAAGATGGATGGATGAACATCTGAATGTCAAATTCCAGACTGGTAGATGTCATTGTGCCAGTCCTG  
GGGATCAAAGAGGGAAAGAGTATTGAGTCAGTCAGTCAACAACTTGTGTTCAAGATGTCAGTCAGTGAATTAT  
TTTCTTCACGTTCTTATCACCACCATGGTTATGTTGGCTGCCCTGCTCACCATTGTTTACTGGGATGTT  
GGTTATATATAATGTTGTTAGCTAAGGTAAGGCTACAGGTCTTACTGACTGGGTGATAAATGAGCTGCCATCATCGACA  
CTTACATTCTTATGACACCAAAGATGCCCTGTTACTGACTGGGTGATAAATGAGCTGCCATCCTCCAGTGGCTGACA  
AGAGCCGAGACAAAAAGCTCTCCTTGTCTAGAGGGAGGGATTGGGACCCGGGATTGGGCATCATCGACA  
TCATGCAGAGCATCAACCAAAGCAAGAAAACAGTATTGTTAAACAAAAAATATGCAAAAGCTGAACTTTA  
AAACAGCTTTTACTTGGTTTGAGGCTACGGCAGGGATCTGTAAGAGCTCCATCCTCCAGTGGCTGACA  
CAGTGTACAGCATTCTCAGTATTGAGGCTACGGCAGGGATCTGTAAGAGCTCCATCCTCCAGTGGCTGACA  
ACCCGAAGGCAGAAGGCTTGGCAAACCTGAGAAATGTTGACTGAAATGATTACGGTATAACA  
ATATGTATGTCGATTCCATTAAAGCAACTAACTGACGTTAGTCATGTTGCGCATAATAAAGATGCAAAG  
GAATGACATTCTGTATTAGTTATGCTATGAAACAAATTATCCAAAACCTAGTGGTTAAACAAACACA  
TTTGTGGCCCACAGTTTGAGGGTCAGGAGTCCAGGCCACGCTAACTGGGTCTCTGCTCAGGGTGTCTCAG  
AGGCTGCAATGTAGGTGTTACCCAGAGACATAGGCATCACTGGGTACACTCATGTGGTTGTTCTGGATTCA  
ATTCTCCTGGCTATTGCCAAAGGCTATACTCATGTAAGGCCATGCCCTCCCACAAGGCAGCTTGCTTC  
ATCAGAGCTAGAAAAAGAGAGGGTTGCTAGCAAGATGAAGTCACAATCTTGTGAAATGCAATCAAAAGTGT  
ATCTCATCACTTGGCCATTCTATTGTTAGAAGTAAACACAGGTCCCACCAAGCTCCATGGGAGTGACC  
TCAGTCCAGGGAAACAGCTGAAGACCAAGATGGTGAGCTCTGATTGCTTCACTGGTCAACTATTTCCT  
TGACTGCTGCTGGGATGGCCTGCTATTGATGATGAGATTGTGAATATCAGGAGGCAGGGATCACTGTGGACC  
ATCTTAGCAGTTGACCTAACACATCTCTTCAATATCTAAGAAACTTTGCCACTGTGACTAATGGCTCTAATA  
TTAAGCTGTTGTTATATTATCATATATCTATGGCTACATGGTTATTATGCTGTGGGTGCGTTGGTTTAT  
TTACAGTTGCTTTACAAATATTGCTGTAACATTGACTCTAAGGTTAGATGCCATTAAAGAACTGAGATGG  
ATAGCTTTAAAGCATCTTTACTCTTACCATTTAAAGTATGCAAGCTAAATTGCAAGCTTTGGCTATA  
TTGTTAATTGCCATTGCTGTAATCTAAAATGAATGAATAAAATGTTCACTTACAAAAA

## FIGURE 211

MENMFLQSSMLTCIFLLISGSCELCAEENFSRSYPCDEKKQNDNSVIAECASNRRLQEVPQTVG  
KYVTELDLSDFITHTNESFQGLQNLTKINLNHNPNVQHQNGNPGIQSNGLNITDGAFLNL  
KNLRELLLEDNQLPQIPSGLPESLTELSLIQNNIYNITKEGISRLINLKNLYLAWNCFNKV  
CEKTNIEDGVFETLTNLELLSLSFNSLSHVPPKLPSSLRKLFLSNTQIKYISEEDFKGLINL  
TLLDLSGNCPRCFNAPFPCVPCDGGASINIDRFAFQNLTQLRYLNLSSTSLRKINAAWFKNM  
PHLKVLDEFNYLVGEIVSGAFLTMLPRLEILDLSFNYIKGSYPQHINISRNFSKLLSLRAL  
HLRGYVFQELREDDFQPLMQLPNLSTINLGINFQKQIDFKLFQNFNLEIIYLSENRISPLV  
KDTRQSYANSSSFQRHIRKRRSTDFFFDPHSNFYHFTRPLIKPQCAAYGKALDLSLNSIFFI  
GPNQFENLPDIACLNLSANSNAQVLSGTEFSAI PHVKYLDLTNNRLDFDNASALTELDLEV  
LDLSYNSHYFRIAGVTHHLEFIQNFTNLKVNLSHNNIYTLDKYNLESKSLVELVFSGNRL  
DILWNDDDNRYISIFKGLKNLTRLDSLNRKHIPNEAFNL PASLTELHINDNMLKFFNWT  
LLQQFPRLELLDLRGNKLLFLTDSDLSDFTSSLRTLLLSHNRISHLPSGFLSEVSSLKHLDLS  
SNLLKTINKSALETKTTKLSMLELHGNPFECTCDIGDFRRWMDEHLNVKIPRLVDVICASP  
GDQRGKSIVSLELTTCVSDVTAVILFFFITTMVMLAALAHHLFYWDVIFIYNVCLAKVK  
GYRSLSTSQTFYDAYISYDTKDASVTDWVINELRYHLEESRDKNVLLCLEERDWDPGLAIID  
NLMQSINQSKKTVFVLTKKYAKSWNFKTAFLALQRLMDENMDVIIFILEPVLQHSQYLR  
RQRICKSSILQWPDNPKAEGLFWQTLRNVVLTENDSRYNNMYVDSIKQY

**Signal sequence:**

amino acids 1-26

**Transmembrane domain:**

amino acids 826-848

## **FIGURE 212**

CCAGGTCCAAC TGACACTCGGTTCTATCGATTGAATTCCCCGGGATCCTCTAGAGATCCCT  
CGACCTCGACCCACCGCGTCCGCCAAGCTGGCCCTGCACGGCTGCAAGGGAGGCTCCTGTGGA  
CAGGCCAGGCAGGTGGCCTCAGGAGGTGCCTCAGGCGGCCAGTGGCCTGAGGCCAGC  
AAGGGCTAGGGTCCATCTCCAGTCCCAGGACACAGCAGCGGCCACCATGGCCACGCCTGGC  
TCCAGCAGCATCAGCAGCCCCCAGGACCGGGAGGCACAGGTGGCCCCCACCACCCGGAGGA  
GCAGCTCCTGCCCTGTCCGGGGATGACTGATTCTCCTCCGCCAGGCCACCCAGAGGAGAA  
GGCCACCCCCGCTGGAGGCACAGGCCATGAGGGGCTCTCAGGAGGTGCTGCTGATGTGGCTT  
CTGGTGTTGGCAGTGGCGGCACAGAGCACGCCAACGGCCGGCGTAGGGTGTGCTGT  
CCGGGCTCACGGGACCCCTGTCTCCGAGTCGTTGTGCAGCGTGTGTACCAAGCCCTCCTCA  
CCACCTGCACGGCACCGGCCCTGCAGCACCTACCGAACCATCTATAGGACGCCAACCGC  
CGCAGCCCTGGCTGGCCCTGCCAGGCCTCGCTACCGGTGCTGCCCGGCTGGAAGAGGAC  
CAGCGGGCTTCCTGGGGCTGTGGAGCAGCAATATGCCAGCCCATGCCGAACGGAGGGA  
GCTGTGTCCAGCCTGGCGCTGCCCTGCAGGATGGCGGGGTGACACTTGCCAGTCA  
GATGTGGATGAATGCAGTGCTAGGAGGGCGGCTGTCCCCAGCGTGCATCAACACCGCCGG  
CAGTTACTGGTGCAGTGTGGAGGGCACAGCCTGTGCAGACGGTACACTCTGTGTGC  
CCAAGGGAGGGCCCCCAGGTGGCCCCAACCGACAGGAGTGGACAGTGCAATGAAGGAA  
GAAGTGCAGAGGCTGCAGTCCAGGGTGGACCTGCTGGAGGAGAAGCTGCAGCTGGTGTGGC  
CCCACTGCACAGCCTGGCCTCGCAGGCACTGGAGCATGGCTCCGGACCCGGCAGCCTCC  
TGGTGCACTCCTCCAGCAGCTGGCCGCATCGACTCCCTGAGCGAGCAGATTCCCTCCTG  
GAGGAGCAGCTGGGGCTGCTCCTGCAAGAAAGACTCGTGACTGCCAGCGCCCCAGGCTG  
GACTGAGCCCTCACGCCGCCCTGCAGCCCCATGCCCTGCCAACATGCTGGGGTCCAG  
AAGCCACCTGGGGTGAUTGAGCGGAAGGCCAGGCAGGGCTTCCTCTTCCCTCCCC  
TTCTCGGGAGGCTCCCCAGACCCCTGGCTACCCCAACGGCATCCAAAGGCCAGGTGGCCCTCAGCTG  
AGGAAGGTACGAGCTCCCTGCTGGAGCCTGGACCCATGGCACAGGCCAGGCAGCCGGAG  
GCTGGGTGGGGCCTCAGTGGGGCTGCTGCCTGACCCCCAGCACAATAAAATGAAACGTGA  
AAAAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGCGACTCTAGAGT  
CGACCTGCAGAAGCTGGCCGCATGGCCAACCTGTTATTGCAGCTTATAATGGTTACAAAT

## **FIGURE 213**

MRGSQEVL LMWLLVIAVGGTEHAYRPGR RVCAVRAHGD PVSE SFVQR VYQPFLTTCDGHRAC  
STYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQPGRCR  
CPAGWRGDTCQSDVDEC SARRGGCPQRCINTAGSYWCQCWE GHSL SADGTL CVPKG GPPRVA  
PNPTGVDSAMKEEVQRLQSRVLLEEK LQLVLA PLHSL ASQALEHGLPD PGSL LVHSF QQLG  
RIDSLSEQISFLEEQLGSCSCKKDS

**Signal sequence:**

1-19

## **FIGURE 214**

GCCAGGCAGGTGGCCTCAGGAGGTGCCCTCAGGCAGGCCAGTGGCCTGAGGCCAGCAAG  
GGCTAGGGTCCATCTCCAGTCCCAGGACACAGCAGCGGCCACCATGCCACGCCTGGCTCC  
AGCAGCATCAGAGCAGCCCTGTGGTGGCAGCAAAGTCAGCTGGCTGGCCCTGTGA  
GGGGCTTCGCGCTACGCCCTGCGGTGCCCCAGGGCTGAGGTCTCCTCATCTTCTCCCTAGC  
AGTGGATGAGCAACCCAACGGGGCCGGGAGGGAACTGGCCCCGAGGGAGAGGAACCCC  
AAAGCCACATCTGTAGCCAGGATGAGCAGTGTGAATCCAGGCAGCCCCCAGGACCGGGAGG  
CACAGGTGGCCCCCACCACCCGGAGGAGCAGCTCCTGCCCTGTCCGGGGATGACTGATT  
TCCTCCGCCAGGCCACCCAGAGGAGAAGGCCACCCGCCCTGGAGGCACAGGCCATGAGGGC  
TCTCAGGAGGTGCTGCTGATGTGGCTCTGGTGGCAGTGGCGACAGAGCACGCC  
CCGGCCCGGCCGTAGGGTGTGCTGCCGGCTCACGGGACCCCTGTCTCCAGTCGTT  
TGCAGCGTGTGTACCAAGCCCTCCTCACACCTGCGACGGCACCGGCCCTGCAGCACCTAC  
CGAACCATCTATAGGACCGCCTACCGCCGCAGCCCTGGCTGGCCCTGCCAGGCC  
CGCGTGCTGCCCGGCTGGAAGAGGACCAGCAGGGCTTCCTGGGGCTGTGGAGCAGCAATAT  
GCCAGGCCCATGCCGAACGGAGGGAGCTGTGTCCAGCCTGCCGCTGCCGTGCC  
GGATGGCGGGGTGACACTGCCAGTCAGATGTGGATGAATGCAGTGCTAGGAGGGCGGCTG  
TCCCCAGCGCTGCATCAACACCGCCGGCAGTTACTGGGCCAGTGTGGAGGGCACAGCC  
TGTCTGCAGACGGTACACTCTGTGTGCCAAGGGAGGGCCCCCAGGGTGGCCCCAACCG  
ACAGGAGTGGACAGTGAATGAAGGAAGAAGTGCAGAGGCTGCAGTCCAGGGTGGAC  
GGAGGAGAAGCTGCAGCTGGTGTGCCAGCCTGGCCCTGCAGGCC  
ATGGGCTCCGGACCCGGCAGCCTCTGGTGCAGCTCCTCCAGCAGCTGGCCGC  
TCCCTGAGCGAGCAGATTCTCTGGAGGAGCAGCTGGGTCTGCTCTGCAAGAAAGA  
CTCGTGACTGCCAGCGCTCAGGCTGGACTGAGCCCTCACGCC  
CCCCTGCCAACATGCTGGGGTCCAGAACGCCACCTCGGGGTGACTGAGCGGAAGGCC  
AGGGCTTCCTCCTCTCCCTCCCTGGGAGGCTCCCCAGACCC  
GGGCTGGATCTCTGTGAATCCACCCCTGGCTACCCCCACCC  
TCCCAAGGCCAGGTGGACCCCTCAGCTGAGGGAGGTAC  
CCATGGCACAGGCCAGGCAGCCGGAGGCTGGGTGGGGCTCAGTGGGGCTGCTGCC  
CCCCAGCACAATAAAATGAAACGTG

## **FIGURE 215**

MRGSQEVLLMWLLVIAVGGTEHAYRPGRVCVRAGDPVSESFVQRVYQPFLTTCDGHRAC  
STYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQPGRCR  
CPAGWRGDTCQSDVDECSARRGGCPQRCINTAGSYWCQCWEGHLSADGTLCVPKGGPPRVA  
PNPTGVDSAMKEEVQRLQSRVDLLEEKQLVLAPLHSLASQALEHGLPDPGSLLVHSFQQLG  
RIDSLSEQISFLEEQLGSCSCKDS

**Signal sequence:**

1-19

## **FIGURE 216**

CCACCGCGTCCGAAGCTGGCCCTGCACGGCTGCAAGGGAGGCTCCTGTGGACAGGCCAGGCA  
GGTGGGCCTCAGGAGGTGCCTCCAGGCCAGTGGCCTGAGGCCAGCAAGGGCTAGGG  
TCCATCTCCAGTCCCAGGACACAGCAGCGGCCACCATGCCACGCCCTGGCTCCAGCAGCAT  
CAGCAGCCCCCAGGACCGGGAGGCACAGGTGGCCCCACCACCCGGAGGAGCAGCTCCTGC  
CCCTGTCCGGGGATGACTGATTCTCTCCGCCAGGCCACCCAGAGGAGAAGGCCACCCGC  
CTGGAGGCACAGGCC**TGAGGGCTCTCAGGAGGTGCTGCTGATGTGGCTCTGGTGTGGC**  
AGTGGGCGGCACAGAGCACGCCAACCGGCCGGCGTAGGGTGTGCTGTCGGGCTCACG  
GGGACCCCTGTCTCCGAGTCGTTCGCAGCGTGTGTACCGCCCTCCTCACCAACCTGCGAC  
GGGCACCGGGCCTGCAGCACCTACCGAACCATCTATAGGACCGCCTACCGCCGAGCCCTGG  
GCTGGCCCTGCCAGGCCTCGCTACCGTGTGCCCCGGCTGGAAGAGGACCAGCAGGGCTTC  
CTGGGGCCTGTGGAGCAGCAATATGCCAGCCATGCCGGAACGGAGGGAGCTGTGTCAG  
CCTGGCCGCTGCCGCTGCCCTGCAGGATGGCGGGGTGACACTTGCCAGTCAGATGTGGATGA  
ATGCAGTGCTAGGAGGGCGGCTGTCCCCAGCGCTGCGTCAACACCGCCGGCAGTTACTGGT  
GCCAGTGTTGGAGGGCACAGCCTGTGCAAGACGGTACACTCTGTGTGCCAACAGGGAGGG  
CCCCCCAGGGTGGCCCCAACCGACAGGAGTGGACAGTGAATGAAGGAAGAAGTGCAGAG  
GCTGCAGTCCAGGGTGGACCTGCTGGAGGAGAACGCTGCAGCTGGTGTGGCCCCACTGCACA  
GCCTGGCCTCGCAGGCAGTGGAGCATGGCTCCCGACCCGGCAGCCTCTGGTGCAGTCC  
TTCCAGCAGCTGGCCGCATCGACTCCCTGAGCGAGCAGATTCTCTGGAGGAGCAGCT  
GGGTCTGCTCTGCAAGAAAGACTCG**TGACTGCCAGCGCCCCAGGCTGGACTGAGCCCC**  
TCACGCCGCCCTGCAGCCCCATGCCCTGCCAACATGCTGGGGTCCAGAACGCCACCTCG  
GGGTGACTGAGCGGAAGGCCAGGCAGGGCTTCCTCTTCCCTCCCTCCTCGGGAG  
GCTCCCCAGACCCCTGGCATGGATGGATGGCTGGATCTTCTCTGTGAATCCACCCCTGGCTACC  
CCCACCCGGCTACCCCAACGGCATCCAAAGGCCAGGTGGCCCTCAGCTGAGGAAAGGTAC  
GAGCTCCCTGCTGGAGCCTGGACCCATGGCACAGGCCAGGCAGCCGGAGGCTGGGTGGGG  
CCTCAGTGGGGCTGCTGCCTGACCCCCAGCACAATAAAATGAAACGTG

## **FIGURE 217**

MRGSQEVLIMWLLVLAvggTEHAYRPGRRVCAVRAHGDPVSESFVQRVYQPFLTCDGHRA  
STYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQPGRCR  
CPAGWRGDTQCSDVDECSARRGGCPQRCVNTAGSYWCQCWEGHSLADGTLCVPKGGPPRVA  
PNPTGVDSAMKEEVQRLQSRVLLEEKLQLVLAPLHSLASQALEHGLPDPGSLLVHSFQQLG  
RIDSLSEQISFLEEQLGSCSCKKDS

**Signal sequence:**

1-19

## **FIGURE 218**

GGTTGCCACAGCTGGTTAGGGCCCGACCACGGGGCCCTTGTCAAGGAGGAGACAGCCTCCGGCCGGGGAG  
GACAAGTCGCTGCCACCTTGGCTGCCACGTGATTCCCTGGACGGTCCGTTCCCTGCCGTAGCTGCCGGCCG  
AGTTGGGTCTCCGTTTCAAGGCCGCTCCCCCTTCTGGTCTCCCTCTCCCGTGGCCGGTTATCGGGAGG  
AGATTGTCTTCCAGGGCTAGCAATTGGACTTTGATGATGTTGACCCAGCGGCAGGAATAGCAGGAACAGTGAT  
TTCAAAGCTGGGCTCAGCCTGTGTTCTCTCGTGTAAAGCAGGAAATGGGAGAAACTCCCAGGCAGGAACACCTTTGCTGTG  
A  
T  
ATGGCCGCGTCATGATGCCCGAAAAGGGATTTCTACCTGACCCCTTCTCATCTGGGACATGTACAC  
TCTCTTCGCTTGTGAGTGCCGTAACCTGGCTGTTCACTGTCCTGCCATCCGTATTCGCTGCCATGCTCT  
TCCCTTCTCCATGGCTACACTGTTGAGGACAGCTTCAGTGACCCGGAGTGATTCCCTGGGCGTACAGATG  
AAGCAGCTTCATAGAAATGGAGATAGAACGTTACCAATGGTGCAGGCCCCAGGGCCAGCGACCACGCCCTCGTA  
TCAAGAATTCCAGATAAACAAACCAGATTGTGAAACTGAAATACTGTTACACATGCAAGATCTTCCGGCTCCCC  
GGGCCTCCATTGCAGCATCTGTGACAACCTGTTGAGGACGCTTCGACCATCACTGCCCTGGTGGGAATTGTG  
TTGGAAAGAGGAACCTACCGCTACTCTACCTCTCATCCTTCTCTCCCTCACAATCTATGCTTCCGCT  
TCAACATCGTCTATGTGCCCTAAATCTTGAAAATTGGCTTCTGGAGACATTGAAAGAAACTCCTGGAACTG  
TTCTAGAAGTCTCATTGCTTCTTACACTCTGGCCGTGGACTGACTGGATTTCATACTTCCCTCGTGG  
CTCTCAACCAGACAACCAATGAAGACATCAAAGGATCATGGACAGGGAAAGATCGGTCCAGAACCTACAGCC  
ATGGCAATATTGTGAAGAACTGCTGTGAAGTGCTGTGTTGGCCCTTGCCCCCAGTGTGCTGGATGAAGGGTA  
TTTGCCACTGGAGGAAGTGGAAAGTCGACCTCCCAGTACTCAAGAGACAGTAGCAGCCTCTTGCCACAGAGCC  
CAGCCCCCACAGAACACCTGAACTCAAATGAGATGCCGAGGACAGCAGCACTCCGAAGAGATGCCAACCTCCAG  
AGCCCCCAGGCCACACAGGAGGAGCTGAAGCTGAGAAGTAGCTATCTATGGAAGAGACTTTGTTGTGTT  
TAATTAGGGCTATGAGAGATTTCAGGTGAGAAGTTAAACCTGAGACAGAGAGCAAGTAAGCTGTCCTTTAACT  
GTTTTCTTGGCTTGTAGTCACCCAGTGTGACACTGGCATTCTGCTGCAAGCTTTAAATTCTGAACCT  
CAAGGCAGTGGCAGAACAGATGTCAGTCACCTCTGATAACTGGAAAAATGGGTCTTGGCCCTGGCACTGGTTCT  
CCATGGCCTAGCCACAGGGTCCCCCTGGACCCCTCTTCCCTCAGATCCCAGCCCTGGCTGGGTAC  
TGGTCTCATTCTGGGCTAAAAGTTTGAGACTGGCTCAAATCTCCCAAGCTGCTGCACGTGCTGAGTCCAGA  
GGCAGTCACAGAGACCTGGCCAGGGATCTTAACGGTTCTGGGTCTTCAGGACTGAAGAGGAGGAG  
TGGGGTCAGAAGATTCTCTGGCACCAAGTGCAGCATTGCCACAAATCCTTTAGGAATGGGACAGGTACCT  
TCCACTTGTGTTGANNNNNNNNNNNNNNNNNNNNNNNTGTTTTCTTGTACTCTGCTCCATTAGGAG  
CAGGAATGGCAGTAATAAAAGTCTGACTTTGGTCAATTCTTCCCTCAGAGGAAGCCGAGTGCTCACTTAAAC  
ACTATCCCCTCAGACTCCCTGTGTGAGGCCTGCAGAGGCCCTGAATGCACAAATGGAAACCAAGGCACAGAGAG  
GCTCTCCTCTCCTCTCCCTCTCCCCGATGTACCTCAAAAAAAAAAATGCTAACCAAGTCTTCCATTAAGCCT  
CGGCTGAGTGAGGGAAAGCCCAGCACTGCTGCCCTCTGGGTAACTCACCCCTAACGGCCTGGCCACCTCTGGCT  
ATGGTAACCACACTGGGGCTTCCCAAGCCCCGCTTCCAGCATTCCACCGCAGAGTCCCAGAGCCACTT  
CACCCCTGGGGTGGCTGTGGCCCCAGTCAGCTGTGCTCAGGACCTGCTTATTCAGGAAAGAAGATTATGT  
ATTATATGTGGCTATATTCTAGAGCACCTGTGTTTCTCTTCTAAGCCAGGTCTGTCTGGATGACTTAT  
GCGGTGGGGAGTGTAAACCGAACCTTCATCTATTGAAGGCGATTAAACTGTGTCTAATGCA

## **FIGURE 219**

MSVMVVRKKVTRKWEKLPGRNTFCCDGRVMMARQKGIFYLTLFLILGTCTLFFAFECRYLAV  
QLSPAIPVFAAMLFLFSMALLRTSFSDPGVIPLAPDEAAFIEMEIEATNGAVPQGQRPPP  
RIKNFQINNQIVKLKYCYTCKIFRPPRASHCSICDNCVERFDHHCPWVGNCVGKRNRYRYFYL  
FILSLSLLTIYVFVNIVYVALKSLKIGFLETLKETPGTVLEVLIKFFTWSVVGILTGFHTF  
LVALNQTTNEDIKG SWTGKNRVQNPySHGNIVKNCCEVLCGPLPPSVLDRRGILPLEESGSR  
PPSTQETSSSLLPQSPAPTEHLNSNEMPEDSSTPEEMPPEPPPEPQEAAEAEK

**Putative transmembrane domains:**

amino acids 36-55 (type II TM), 65-84, 188-208, 229-245

## **FIGURE 220**

AAAACCCTGTATTTTACAATGCAAATAGACAATNANCCTGGAGGTCTTGAAATTAGGTAT  
TATAGGGATGGTGGGGTTGATTTTNTTCCTGGAGGCTTGGACTCTCNCTTCT  
CCCACAGAGCNCTCGACCATCACTGCCCTGGGTGGGAATTGTGTTGGAAAGAGGAACTA  
CCGCTANTTCTACCTCTTCATCCTTNTCTCTCCNCCTCACAAATCTATGTCTCGCCTTCA  
ACATCGT

## **FIGURE 221**

GTTGTGTCCTTCAGCAAAACAGTGGATTAAATCTCCTGCACAAGCTTGAGAGCAACACAA  
TCTATCAGGAAAGAAAGAAAGAAAAAAACCGAACCTGACAAAAAAGAAGAAAAGAAGAAGA  
AAAAAAATCATGAAAACCATCCAGC~~AAA~~ATGCACAATTCTATCTCTGGGCAATCTTCAC  
GGGGCTGGCTGCTCTGTCTCTTCCAAGGAGTGCCC GTGCGCAGCGGAGATGCCACCTTCC  
CCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGAGAGCGCCACCTCAGGTGCACTATT  
GACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGA  
CAAGTGGTGCCTGGATCCTCGCGTGGCCTCTGAGCAACACCCAAACGCAGTACAGCATCG  
AGATCCAGAACGTGGATGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACAAAC  
CACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCAAAATTGTAGAGATTT  
TTCAGATATCTCCATTAATGAAGGGAAACAATATTAGCCTCACCTGCATAGCAACTGGTAGAC  
CAGAGCCTACGGTTACTTGGAGACACATCTCTCCAAAGCGGTTGGCTTGAGTGAAGAC  
GAATACTTGGAAATTCAAGGCATCACCCGGGAGCAGTCAGGGACTACGAGTGCAGTGCCTC  
CAATGACGTGGCCGCCGTGGTACGGAGAGTAAAGGTACCCTGAACATCCACCATACA  
TTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGACAAAAGGGACACTGCAGTGTGAAGCC  
TCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAAAGACTGATTGAAGGAAA  
GAAAGGGGTGAAAGTGGAAACAGACCTTCCCTCTCAAAACTCATCTTCTCAATGTCTTG  
AACATGACTATGGAAACTACACTTGCCTGGCCTCCAACAAGCTGGCCACACCAATGCCAGC  
ATCATGCTATTGGTCCAGGCGCCGTAGCGAGGTGAGCAACGGCACGTGAGGAGGGCAGG  
CTGCGTCTGGCTGCTGCCTTTCTGGTCTTGACCTGCTTCTCAAATTTGATGTGAGTGCC  
ACTTCCCCACCCGGAAAGGCTGCCACCACCAACACAGCAATGGCAACAC  
CGACAGCAACCAATCAGATATATAACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGA  
AATTGAGGGAGGGAAACAAAGAATACTTGGGGGGAAAAGAGTTAAAAAGAAATTGAA  
AATTGCCTTGCAGATATTAGGTACAATGGAGTTTCTTCCAAACGGGAAGAACACAGC  
ACACCCGGCTGGACCCACTGCAAGCTGCATCGTGCACCTCTTGGTGCCAGTGTGGGCAA  
GGGCTCAGCCTCTGCCACAGAGTGCCCCACGTGGAACATTCTGGAGCTGGCCATCCCA  
AATTCAATCAGTCCATAGAGACGAACAGAATGAGACCTCCGGCCAAGCGTGGCGCTGCGG  
GCACTTGGTAGACTGTGCCACCACGGCGTGTGAAACGTGAAATAAAAGAGCAAAA  
AAAAA

## **FIGURE 222**

MKTIQPKMHNSISWAIFTGLAALCLFQGPVRSGDATFPKAMDNVTVRQGESATLRCTIDNR  
VTRVAWLNRSTILYAGNDKWCLDPRVLLSNTQTQYSIEIQNVDVYDEGPYTCVQTDNHPK  
TSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVWRHISPKAVGFVSEDEYL  
EIQGITREQSGDYECSASNDVAAPVVRRVKVTVNYPPIISEAKGTGVPVGQKGTLQCEASAV  
PSAEFQWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNLGHTNASIML  
FGPGAVSEVSNNGTSRRAGCVWLLPLLVLHLLLKF

**Signal peptide:**

amino acids 1-28

## **FIGURE 223**

GAAAAAAAATCATGAAAACCATCCAGCCAAAATGCACAATTCTATCTCTGGGCAATCTTC  
ACGGGGCTGGCTGCTCTGTCTCTTCCAAGGAGTGCCCCGTGCGCAGCGGAGATGCCACCTT  
CCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGAGAGGCCACCTCAGGTGCACTA  
TTGACAACCGGGTCACCCGGGTGGCTAAACCGCAGCACCATCCTATGCTGGGAAT  
GACAAGTGGTGCCTGGATCCTCGCGTGGCCTTCTGAGCAACACCCAAACGCAGTACAGCAT  
CGAGATCCAGAACGTGGATGTGTATGACGAGGCCCTAACACCTGCTCGGTGCAGACAGACA  
ACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCAAAATTGTAGAGATT  
TCTTCAGATATCTCCATTAATGAAGGAAACAATATTAGCCTCACCTGCATAGCAACTGGTAG  
ACCAGAG

## FIGURE 224

ATGGCTGGTACGGCGGGCGGGCAGGGGACCGGGGCCGGCCGGAGCGGGCAGCTGCCGGAGCCCTGA  
ATCACCGCCTGCCCGACTCCACC**AT**GAACGTGCCTGCAGGAGCTGGAGCTGCAGCAACGTGGATTCCAG  
AAGGGGACAAGAACAGCTGTTAGGCTACGCACGCAGCTGGAGCTGGCTTAGCAGGTGCCTCTACTGCTGGCT  
GCACTGCTCTGGGCTGCCCTGTGCCCTAGGGTCCAGTACCAAGAGACCCATCCCACAGCACCTGCCCTACA  
GAGGCCTGCATTGAGTGGCTGGAAAAATCCTGGAGTCCTGGAGCGAGGGTGGAGCCCTGTGAGGACTTTAC  
CAGTCTCCTGTGGGGCTGGATTGGAGAACCCCTGCCATGGCCTCTCGCTGGAAACACCTCAACAGC  
CTCTGGGACAAAACCAGGCCATACTGAAGCACCTGCTGAAAACACCACTCAACTCCAGCAGTGAGCTGAG  
CAGAAGACACAGCCTCTACCTATCTGCCATCAGGTGGAGCGCATTGAGGAGCTGGAGCCAGCCACTGAGA  
GACCTCATTGAGAAGATTGGTGGTGGAAACATTACGGGCCCTGGGACCAGGACAACATTATGGAGGTGTTGAAG  
GCAGTAGCAGGGACCTACAGGCCACCCATTCTTCAACGCTACATCAGTGCCTACTAAGAGTTCCAACAGC  
AATGTTATCCAGGTGGACCACTGCTGGCTCTTCTGCCCTCTGGGATTACTACTAAACAGAACTGCCAATGAG  
AAAGTGCTCACTGCCATCTGGATTACATGGAGGAACGGGATGCTGCTGGGTGGCGGCCACCTCACGAGG  
GAGCAGATGCAGCAGGTGCTGGAGTGGAGATAAGCTGCCAACATCACAGTGCCTCAGGACCAGCGCGCAG  
GAGGAGAAGATCTACCAAGATGAGCATTGGAGCTGCAGGCTCTGGCGCCCTCCATGGACTGGCTTGAGTTC  
CTGTCTTCTTGCTGTACCATTGGAGTTGAGTGAATCTGAGCCTGTGGTGTATGGGATGGATTATTCAG  
CAGGTGTAGAGCTCATCAACCGCACCGAACAGCATCTGAACAATTACCTGATCTGGAAACCTGGTGC  
ACAACCTCAAGCCTGGACCGACGCTTGAGTCTGCACAAGAGAACGCTGGAGACCCCTCATGGCACA  
TCCTGTGTGCCAGGTGGCAGACCTGCATCTCAAACACGGATGACGCCCTGGCTTGCTGGGTCACTCTC  
GTGAAGGCCACGTTTGACCGCAAAGCAAAGAAATTGCAAGGGGATGATCAGCGAAATCCGGACCGCATTGAG  
GAGGCCCTGGGACAGCTGGTTGGATGGATGACAAGACCCGCCAGGAGCAGCAAGGAGAAAGCAGATGC  
GATATGATTGGTTCCGACCTTATCTGGAGCCAAAGAGCTGGATGATGTTATGACGGGTACGAAATTCT  
GAAGATTCTTCTCCAAAACATGTTGAATTGTAACCTCTCTGCCAAGGTTATGGCTGACCAGCTCGCAAG  
CCTCCCAGCCGAGACCAGTGGAGCATGACCCCCCAGACAGTGAATGCTACTACCTCCAACAGAATGAGATC  
GTCTCCCCGCTGGCATCTGCAGGCCCTCTATGCCGCAACCACCCAGGCCCTGAACCTCGGTGGC  
GGTGTGGTCACTGGGCACTGAGTTGACGCATGCCATTGATGACCAAGGGCGAGTATGACAAAGAAGGG  
CGGCCCTGGTGCAGAATGAGTCCCTGGCAGCCTCCGGAACACACGGCTGCATGGAGGAACACTACA  
TACCAAGGTCAATGGGGAGGGCTCAACGGCCGCCAGACGCTGGGGAGAACATTACTGACA  
ACGGGGGCTGAAG GCTGCCCTACAAAGCATGGCTGAGAAAGCATGGGGAGGGAGCAGCAACTGCC  
AGCGTGGCCTACAAAGCATGGCTGAGAAAGCATGGGGAGGGAGCAGCAACTGCC  
AACCAACCAAGCTCTCTCGTGGGATTGCCAGGTGTGGCTCGTCCGCACACCAGAGAGCT  
CTGGTGACCGACCCCCACAGCCCTGCCGCTTCCGCGTGTGGCAGCTCTCCA  
CACTCGGCTGCCCTGTGGCTCCCCATGAACCCAGGGCAGCTGTGAGGTGTGG**TAG**A  
GAAATGGCCAGCTGTCAACAGACCTGGGGAGCTCTCTGACAAAGCTGTTGCTCTGGGTGGAGGAAGCAA  
ATGCAAGCTGGCTGGGTCTAGTCCCTCCCCACAGGTGACATGAGTACAGACCC  
CTGCCTCTGCTTGGGGTGCCCTGCCAGCAGAGCCCCCACCATTCACTGT  
GCACATCTTCCGTGTCACCC  
GCCTGGAAGAGGTCTGGTGGGGAGGCCAGTCCC  
TAGGAAGGAGTCTGCC

## **FIGURE 225**

MNVALQELGAGSNVGFQKGTRQLLGSRSQLLELVLAGASLLLALLGCLVALGVQYHRDPSH  
STCLTEACIRVAGKILESLDRGVSPCEDFYQFSCGGWIRRNPPLPDGRSRWNTFNSLWDQNQA  
ILKHLLENTTFNNSSEAEQKTQRFYLSCLQVERIEELGAQPLRDLIEKIGGWNIITGPWDQDN  
FMEVLKAVAGTYRATPFFTYYISADSKSSNSNVIQVDQSGFLPLPSRDYYLNRTANEKVLTAY  
LDYMEELGMILLGGRPTSTREQMQQVLELEIQLANITVPQDQRRDEEKIYHKMSISELQALAP  
SMDWLEFLSFLLSPLELSDSEPVVVYGMMDYLQQVSELINRTEPSILNNYLIWNLVQKTTSSL  
DRRFESAQEKLLETLYGTTKSCVPRWQTCISNTDDALGFALGSLFVKATFDRQSKEIAEGMI  
SEIRTAFFEEALGQLVWMDEKTRQAAKEKADAIYDMIGFPDFILEPKELDDVYDGYEISEDSF  
FQNMLNLYNFSAKVMADQLRKPPSRDQWSMTPQTVNAYYLPTKNEIVFPAGILQAPFYARNH  
PKALNFGGIGVVMGHELTHAFDDQGREYDKEGNLRPWQNESLAAFRNHTACMEEQYNQYQV  
NGERLNGRQTLGENITDNGGLKAAYNAYKAWLRKHGEEQQLPAVGLTNHQLFFVGFAQVWCS  
VRTPESSHEGLVTDPHSPARFRVLGTLNSRDFLRHFGCPVGSPMNPGQLCEVW

Type II Transmembrane domain:

amino acids 32-57

## **FIGURE 226**

GCCCCGCCCTCGCCCTCCGCACTCCCCTCCCTCCGCCGCTCCGCCGCCCCCTCCCTCCCTCCCTCC  
CAGCTGTCCCCTTCGCGTCATGCCGAGCCTCCGCCGCCGGCCGCTGCTGCTCCTCGGGCTGCTGCTGCT  
CGGCTCCCGGCCGCCGCCGGCCGAGGCCCGGGCTGCTGCCCATCCGTTCTGAGAAGGAGCCGCTGCC  
CGTTCGGGGAGCGGCAGGTAGGTGGCGCCGGGGAGGGCGGGGGAGTGGGGCTGGGGAGTCAGGCC  
CAGCCCGAGGGGGCGGGCGCAGGTGGCTCGGCCGGGGGGAGGGGGAGGGGGAGTCAGGCC  
GCGGTGCCCTGGGACCCGGACCCGCCGGCAGCCCCGGGGAGCAGCTGGGAGCTGGGAGCAGGCC  
CAAGCCCGTCCCGCAGGTGACCTTCGGCGGAAGGTCTATGCCCTGGACAGACGTGGCACCCGACCTAGG  
GGAGGCCATTGGGGTGATGCCGCTGGCTGTGCGCCTGCGAGGGCAGTGGGTGCGCTTACAGGGCCCTGG  
CAGGGTCAGCTGCAAGAACATCAAACCAGAGTGCCAACCCGGCTGTGGGAGCCGCGCAGCTGCCGGACA  
CTGCTGCCAGACACTGCCCTCAGGACTTCGTTGGCGCTGTCAGGGCCAGGTGCAAGGGCGTGGCACAGGCC  
AGTCTCGCTGCGCTCTAGCCTCCGTTCTATCCTACAGGCCGCTGGACCCCTACAGGATCCGCTT  
CTCAGACTCCAATGGCAGTGTCTGTTGAGCACCCCTGCAAGCCCCACCCAAGATGGCTGGTCTGTGGGTGTG  
GCCGGCAGTGCCTCGGTTGCTCTGCCGCTCTAGGGCAGAACAGCTGCACTGGGACITGTGACACTCACTCA  
CCCTCAGGGGAGGTCTGGGGCCCTCTATCCGGCACCGGGCCCTGTCCTCCAGAGACCTTCAGTGCCATCCTGAC  
TCTAGAAGGCCCCACCAGCAGGGCGTAGGGGCATCACCTGTCACTCTCAGTGAACAGGACTCCTTGCA  
TTTTTGCTGCTCTTCCGAGGCCCTTGCAAGGACTAACCCAGGTTCCCTGAGGCTCCAGATTCTACACCAGGGCA  
GCTACTCGGAAACTTCAGGCCAATGCTCAGGCCAGGAACAGGCTTGTGAGGTGCTGCCAACCTGACAGT  
CCAGGAGATGGACTGGCTGGTCTGGGGAGCTGAGGCTGGCAGGAGGGCAGGGCTGCGCAT  
CAGTGGACACATTGCTGCCAGGAAGAGCTGCCAGCTGCAAAAGTGTCTTGTGGGCTAATGCCCTGATCCC  
AGTCCAAACGGGTCTGCCGCTCACGCCCCACTCTGCTAGGAAATGGCNCCCTGATCTCCAGGTGCAATT  
GGTAGGGACAACAGTGGGTGGCATGCACTGGAAACCAAGGCTCAGGCCAGGGATGCCACTGTCTT  
GTGCCACATGGCTGGCTATCTCCCTGCCCTCAGGGCTGGGTATCTGCCCTGGCTGGGTGCCAGGGGG  
TCATATGCTGCTGCAAGATGAGCTCTTCTGAACTGTCAGGGCACCAAGGACTTCCCAGACGGAGAGCTTGGGGCA  
ACGTGGCTGCCCTGCCCTACTGTGGGCATAGGCCCGCCCTGCCCTAGCAGGAGGCCCTGGTCTACC  
CCCTGTGAAGAGCCAAGCAGCAGGGCACGCCCTGGTTCTGGATAACCACTGTCACCTGCACTATGAAGTGCT  
GCTGGCTGGCTGGTCTGAGAACAGGACTGTCACTGCCAACCTCTGGCCTCTGGAACGCCAGGGC  
TCGGCGCTGCTGAAGGGATTCTATGGCTCAGAGGCCAGGGTGTGGTAAGGACCTGGAGGCCAGCTGCG  
GCACCTGGCAAAAGGATGGCTTCCCTGATGATCACCAAGGTAGCCCAGAGGGGAGCTCGAGGGCAGCCT  
CTCCTCCAGGTGCACTAGCCAACCATGTGAGGTTGGCGACTGCCCTGGAGGGCGCCGGAGGGGG  
GCCGGCGCTGGGGCTCCGGATACAGCCTCTGCTGCCGCGCTGTGGTGCCTGGCTCCGCCAGGCC  
CAAACCTGGTGGTCTGGCGGCCCGAGACCCAAACATGCTTCTCGAGGGCAGCAGGCCACGGGG  
TCGCTGGCGCCAACGACCCGCTCTGCTCACTCTGCACTGCCAGAGACGAACGGTATCTGTGACCCGGT  
GGTGTGCCACCGCCAGCTGCCAACACCCGGTGCAGGCTCCGACCGAGTGTGCCCTGGCTTGGCTGCTGTA  
TTTGATGGTGAACGGAGCTGGGGCAGCGGGTACCGGGTGGCACCCGGTGTGCCCCCTTGGCTTAATTAA  
GTGCTGCTGCTGCAACCTGCAAGCAGGGGGCAGCGGGTACCGGGTGGCACCTGGAGAGGTGACTGAGAAGGTGCA  
CTGTGCCCTGGCTGCTGCAACCCACCGACTGCTGCAAAACAGTGTCCAGGTGAGGCCACCCCCAGCTGG  
GGACCCCATGCAAGGCTGATGGGCCCCGGCTGCCGTTTGCTGGCAGTGGTCCCAGAGAGTCAGAGCTGGCA  
CCCCCTCAGTGCCCTGGTGTGGAGAGATGAGCTGATCACCTGCAAGATGTGGGTAAGTGGGAGCAGAGGCTTGT  
GTGAGGGGGTACTGGAGGCTGGAGTAGGGAGACCTTCCCAGGGAGGTCCCTGAAAGAAGCTGAAGGTCA  
CTGTGTCCCAGTGCCTCTGGGGACACTCAGTGTCTGCTTGTACCGAGCAGGGTGCATGCTGTTCCGCTGCACGCC  
GGGGATGACTGTCACTGCCACTGTCTGCTGGCTGGGAAGGAGAGTCAGTGTGTTCCGCTGCACGCC  
GGCGCGTAAGTGAGGGAGTCCAGGGTCAGCAGCTGTGAGTGGAGGGCTCACCTGCCGTGGAGACTCTGATCAG  
GGAAGGGAGCACTCACTGTGCAAGAACAGTCAGGCCCTACAAGTGCCATTCCAATCCACCCCTCACAGCA  
ACCTGGTGAATTGTTATTGACCTTTCTTACAAATGAGATTCTGAAGCTCAGAGAAAATTAAGCAACGAG  
ATGAAGGTCAACCCAGCTGTGCACTGACCTGTTAGAAAATACTGCCCTTCTGGACCAAGGCAGGGATGCTT  
TGCCCTGCCCTCATGCCCTCTGTGCCCTCTCACTCCCTCCCTCAACATCCCTCCCTCTGTCTCC  
AGCAGCCCCAGAGACCAGAACACTGATCCAGAGAGAACAGGCCAGGGCTTGGAGCAGGCCAGGG  
AAGTGACCAAGAGGATGGGGCTGAGCTGGGGAGGGGGTGGCATCGAGGACCTTCTGCATTCTCTGTGG  
CCCAGTGCCTTGTCTCTGCTGCCCTACTCTCCACCCACTACCTCTGGGAACCAAGCTCCACAAGGG  
GAGAGGCAGCTGGGCCAGACCGAGGTACAGCCACTCCAAGTCAGTCCCTGCCCTGCCACCCCTCG  
GCCACCCCTTCTGTACATAATGTCAGTGGCTGGGATTTTAATTATCTTACTCAGCACCAAG  
GGCCCCGGACACTCCACTCTGCTGCCCTGAGCTGGAGAGTCAGAGTCATTATGGAGAGTTGTATT  
ATTCTTTCTAGTCTGGGATGGGGTGGCTGGGAGAGAGAGTCAGTGGGGAGCTGAAAGAGACCTGG  
GCNGAGAGTAGGGAGGTGAGAGAGAGAGAGTCAGTGGGGAGCTGAAAGAGACCTGGAGAGGGCAGAGG  
CGTGGCNNTGGCTGGCATNCCTGGGAGAGGGCTGGGATGGTTCTGAGATGGTCTAGAGACTCAAG  
AATTAGGGAAAGTAGAACAGGATTGACTCAAGTTAGTTCCACATGCTGCCCTGTTGCTGACTCATG  
TTGAAGTTGCTCCAGAGAGAGAATCAAAGGTGCAACCAGCCCCCTCTCCCTCCCTCCCT  
TCCCTCCCCCTCCCCCTCCCCCTCCCCCTCC

## FIGURE 227

GGCGAGCGGGGTGCTGCAGCGCCGTATGGCTGGTACGGCGGGCGGGCAGGG  
CCGGGGCGCGGCCGGAGCGGCCAGCTGCCGGAGCCCTGAATCACCGCCTGGCCGAC  
TCCACCATGAACGTGCGCTGCAGGAGCTGGAGCTGGCAGCAACGTGGATTCCAGAAGGG  
GACAAGACAGCTGTTAGGCTACGCACGCAGCTGGAGCTGGCTTAGCAGGTGCCTCTAC  
TGCTGGCTGCACTGCTTCTGGCTGCCTTGTGCCCTAGGGTCCAGTACACAGAGACCCA  
TCCCACAGCACCTGCCTACAGAGGCCTGCATTGAGTGGCTGGAAAAATCCTGGAGTCCT  
GGACCGAGGGGTGAGCCCCTGTGAGGACTTTACCAGTTCTCCTGTGGGGCTGGATTCGGA  
GGAACCCCCCTGCCGATGGCGTTCTCGCTGGAACACCTCAACAGCCTCTGGACCAAAAC  
CAGGCCATACTGAAGCACCTGCTTGAAAACACCACCTCAACTCCAGCAGTGAAGCTGAGCA  
GAAGACACAGCGCTTCTACCTATCTTGCCTACAGGTGGAGCGCATTGAGGAGCTGGAGCCC  
AGCCACTGAGAGACCTCATTGAGAAGATTGGTGGTGGAACATTACGGGCCCTGGACCAAG  
GACAACTTATGGAGGTGTTGAAGGCAGTAGCAGGGACCTACAGGGCCACCCATTCTCAC  
CGTCTACATCAGTGCCTACTCTAACAGAGTTCCAACAGCAATGTTATCCAGGTGGACCAGTCTG  
GGCTCTTCTGCCCTCGGGATTACTACTTAAACAGAACTGCCAATGAGAAAGTAAGGAAC  
ATCTTCCGAACCCCCATCCCTACCCCTGGCTGAGCTGGCTGATCCCTGTTGACTTTCCCT  
TTGCCAAGGGTCAGAGCAGGAAGGTGAGCCTATCCTGTACCTAGTGAACAAACTGCCCT  
CCTTCTTCTTCTTCTCCCTCCCTCCCTTTCTCCCTTCCCTTCCCTTCC  
TCTTATTCTCTAGTAGGTTCATAGACACCTACTGTGTGCCAGGTCCAGTGGGGAAATTG  
GAGATATAAGTTCCGAGCCATTGCCACAGGAAGCGTTAGTGTGATGGGTTATGGACCT  
AGATAGGCTGATAACAAAGCTCACAAGAGGGTCTGAGGATTCAAGGAGAGACTTATGGAGCC  
AGCAAAGTCTCCTGAAGAGATTGCATTGAGCCAGGTCTGTAG

## **FIGURE 228**

ATGCCTACTACCTTCCAACAAGAATGAGATCGTCTTCCCCGTGGCATCCTGCAGGCC  
TTCTATGCCCGCAACCACCCCAAGGCCCTGAACCTCGGTGGCATCGGTGTGGTCATGGCCA  
TGAGTTGACGCATGCCTTGATGACCAAGGGCGCGAGTATGACAAAGAACGGGACCTGCGGC  
CCTGGTGGCAGAATGAGTCCCTGGCAGCCTCCGGAACACACGGCCTGCATGGAGGAACAG  
TACAATCAATACCAGGTCAATGGGGAGAGGGCTCAACGGCCGCCAGACGCTGGGGGAGAACAT  
TGCTGACAACGGGGGCTGAAGGCTGCCTACAATGCTTACAAAGCATGGCTGAGAAAGCATG  
GGGAGGAGCAGCAACTGCCAGCCGTGGGCTACCAACCACAGCTCTCGTGGGATT  
GCCAGGTGTGGTGCCTGGTCCGCACACCAGAGAGCTCTCACGAGGGCTGGTGACCGACCC  
CCACAGCCCTGCCGCTTCCCGTGCTGGCACTCTCTCCAACCTCCGTACTTCCTGCGGC  
ACTTCGGCTGCCCTGTCGGCTCCCCATGAACCCAGGGCAGCTGTGAGGTGTGGTAGACC  
TGGATCAGGGGAGAAATGGCCAGCTGTCACCAGACCTGGGCAGCTCTCGACAAAGCTGT  
TTGCTCTTGGGTTGGGAGGAAGCAAATGCAAGCTGGCTGGGTCTAGTCCCTCCCCCACA  
GGTACATGAGTACAGACCCCTCAATCACCAATTGTGCCTCTGCTTGGGGTGCCCCT  
GCCTCCAGCAGAGCCCCACCATTCACTGTGACATCTTCCGTGTCACCCCTGCCTGGAAGAG  
GTCTGGGTGGGAGGCCAGTCCCATAGGAAGGAGTCTGCCTCTGTCCCCAGGCTCACT  
CAGCCTGGCGGCCATGGGCCTGCCGTGCCCTGCCCACTGTGACCCACAGGCCTGGGTGGT  
TACCTCCTGGACTTCTCCCCAGGCTCACTCAGTGCACCTAGGGGTGGACTCAGCTCTGTC  
TGGCTCACCCCTCACGGCTACCCCCACCTCACCCGTGCTCCTGTGCCACTGCTCCAGTG  
CTGCTGCTGACCTTCACTGACAGCTCTAGTGGAAAGCCAAGGGCCTCTGAAAGCCTCCTGC  
TGCCCCACTGTTCCCTGGCTGAGAGGGAAAGTCATATGTGTAGCGGGTACTGGTCCTGT  
GTCTTAGGGCACAAGCCTAGCAAATGATTGATTCTCCCTGGACAAAGCAGGAAAGCAGATA  
GAGCAGGGAAAAGGAAGAACAGAGTTATTTTACAGAAAAGAGGGTGGAGGGTGTGGTCT  
TGGCCCTTATAGGACC

## **FIGURE 229**

CCACCGCGTCCGAGCCGCCGAGAATTAGACACACTCCGGACGCCAAAAGCAACCGAGA  
GGAGGGGAGGCACAAACACCGAAAAACAAAAAGAGAGAAACAACACCCAACTGGGTGG  
GGGAAGAAAGAAAGAAACCCACCCACCAAAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAATCCTGTGGCGCCGCCCTGGTTCCCGGAAAGACTGCCAGCACCGGGG  
TGGGGAGTGCAGCTGAAAGCTGCTGGAGAGTGAGCAGCCCTAGCAGGGATGGAC**ATGATG**  
CTGTTGGTGAGGGTGCAGCTGCTCGAACCAAGCTGGCTGGCGCCGGTGCCTCAGCCTGTG  
CTGCCTGCTACCCCTCGCCTCCGGCTGGACAGAGTGTGGACTTCCCCTGGCGCCGTGG  
ACAACATGATGGTCAGAAAAGGGACACGGCGGTGCTTAGGTGTTATTGGAAGATGGAGCT  
TCAAAGGGTGCCTGGCTGAACCGGTCAAGTATTATTGCGGGAGGTGATAAGTGGTCAGT  
GGATCCTCGAGTTCAATTCAACATTGAATAAAGGGACTACAGCCTCCAGATAACAGAATG  
TAGATGTGACAGATGATGGCCCATAACGTGTTCTGTTAGACTCAACATAACCCAGAAC  
ATGCAGGTGCATCTAAGTGTGCAAGTTCCCTCTAAGATATATGACATCTCAAATGATATGAC  
CGTCAATGAAGGAACCAACGTCACTCTTACTTGTGTTGCCACTGGGAAACCAAGAGCCTCCA  
TTTCTGGCGACACATCTCCCCATCAGCAAAACCATTGAAAATGGACAATATTGACATT  
TATGGAATTACAAGGGACCAGGCTGGGAATATGAATGCAAGTGCAGTGCAGGAAATGCTGTGTCATT  
CCCAGATGTGAGGAAGTAAAGTTGTCACACTTGCTCTACTATTCAAGGAAATTAAAT  
CTGGCACCGTGACCCCCGGACGCAGTGGCTGATAAGATGTGAAGGTGCAGGTGTGCCGCCT  
CCAGCCTTGAATGGTACAAAGGAGAGAAGAAGCTTCAATGCCAACAGGAATTATT  
TCAAAATTAGCACAAGATCCATTCTCACTGTTACCAACGTGACACAGGAGCACTCGGCA  
ATTATACTGTGTGGCTGCCAACAGCTAGGCACAACCAATGCGAGCCTGCCCTTAACCCT  
CCAAGTACAGCCCAGTATGGAATTACCGGGAGCGCTGATGTTCTTCTCTGCTGTTACCT  
TGTGTTGACACTGTCTCTTCACCAGCATATTCTACCTGAAGAATGCCATTCTACA**ATAA**  
TTCAAAGACCCATAAAAGGTTTAAGGATTCTGAAAGTGTGATGGCTGGATCCAATCT  
GGTACAGTTGTTAAAGCAGCGTGGGATATACTCAGCAGTGTACATGGGATGATGCC  
TTCTGTAGAATTGCTCATTATGTAATAACTTTAATTCTACTCTTTTGATTAGCTACATTA  
CCTTGTGAAGCAGTACACATTGCTTTTAAGACGTGAAAGCTCTGAAATTACTTTAG  
AGGATATTAAATTGTGATTTCATGTTGAATCTACAACCTTCAAAAGCATTCACTGATGGT  
CTGCTAGGTTGCAGGCTGAGTTACAAAAGCAATTGCAAGTGAATATGTGATTCTTAA  
GGCTGCAATACAAGCATTCACTGCTTCAATAAGACGTCAATCCACATTACAAGATG  
CATTTTTCTTTTGATAAAAAGCAAATAATTGCTTCAGATTATTCTCAAAATA  
TAACACATATCTAGATTTCTGCTTGCACTGATATTCAAGGTTCAAGGATGAGCCTGTAAT  
ATAACTGGCTGTGCAGCTCTGCTTCTTCTGTAAGTTCACTGATGGGTGTGCCTTCATAC  
AATAATTCTCTTGTCTCCAACATAATAAAATGTTGCTAAATCTACAATTGTA  
AAGTAAAATAAACAGAGTGTCAAGTTAAACCAACTACACTATCTCTAAGTAACGAAGGAGC  
TATTGGACTGTAAAATCTCTTGTGACTGACAATGGGTTGAGAATTGCCCCACACT  
AACTCAGTTCTGTGATGAGAGACAATTAAATAACAGTATAGTAAATACCATATGATTT  
TTTAGTTGTTAGCTAAATGTTAGATCCACCGTGGAAATCTTCAAAATGACAGCACA  
GTCCACTCAAAGGATTGCTTAGCAATACAGCATCTTCTTCACTAGTCCAAGC  
TTTAAGATGATTGTCAGAAAGGGACAAAGCTCTATCACCTAATATTACAAGAGTTGGTA  
AGCGCTCATTAATTATTGTCAGGTTATTATGACAGTCGACCTGGAGGGTATGGA  
TATGGATATGGACGTTCCAGAGACTATAATGGCAGAAACCAGGGTGGTTATGACCGCTACTC  
AGGAGGAAATTACAGAGACAATTGACAACGTGAAATGAGACATGCACATAATAGATA  
CAAGGAATAATTCTGATCCAGGATGTCCTCCAAATGGCTGTTAAAGGTTTTGG  
AGCTGCACTGAAGCATCTTATTTATAGTATCAACCTTGTAAATTGACACTGCCA  
AGTAGCTGAAGACCTTTAGACAGTTCCATCTTTAAATTCTGCTATTAA  
AGACAAATTATGGGACGTTGTCACAAAAAA

## **FIGURE 230**

MMLLVQGACCSNQWLAAVLLSLCCLLPSCLPAGQSVDFFWAAVDNMMVRKGDTAVLRCYLED  
GASKGAWLNRSSIIFAGGDKWSVDPRVSISTLNKRDYSLQIQNVDVTDDGPYTCSVQTQHTP  
RTMQVHLTVQVPPKIYDISNDMTVNEGTVNLTCLATGKPEPSISWRHISPSAKPFENGQYL  
DIYGITRDQAGEYECSAENAVSFDPDVRKVVVNFAPTIQEIKSGTVTPGRSGLIRCEGAGV  
PPPafeWYKGEKKLFNGQQGIIIQNFSTRSILTNTVNTQEHFGNYTCVAANKLGTTNASLPL  
NPPSTAQYGITGSADVLFSCWYLVLTSSFTSIFYLKNAILQ

**Important features of the protein:**

**Signal peptide:**

amino acids 1-31

**Transmembrane domain:**

amino acids 326-345

**N-glycosylation sites.**

amino acids 71-75, 153-157, 273-277, 284-288, 292-296, 305-309

**Casein kinase II phosphorylation site.**

amino acids 147-151, 208-212, 224-228

**Tyrosine kinase phosphorylation site.**

amino acids 178-186

**N-myristoylation sites.**

amino acids 7-13, 63-70, 67-73, 151-157, 239-245, 291-297,  
302-308, 319-325

**Myelin P0 protein:**

amino acids 92-121

## **FIGURE 231**

AGTGGTCGATGGGAAGGATCTTCTCCAAGTGGTCCTTGAGGGAGCATTCTGCTGG  
CTCCAGGACTTGGCATCTATAAGCTGGCAATGAGAAATAAGAAAATTCTAAGGAGGA  
CGAGCTTGTGAGGACCAACAAGCTGCTTCACCAAATTGCAATGGAGCCTTCGAAA  
TCAATGTTCAAAGCCAAGAGGAGAAATGGGGTGAACCTCTCCCTAGCTGTGGTGGTCATC  
TACCTGATCCTGCTACCGCTGGCGCTGGCTGCTGGTGGTCCAAGTTCTGAATCTGCAGGC  
GCGGCTCCGGTCTGGAGATGTATTCCTCAATGACACTCTGGCGGCTGAGGACAGCCCCTG  
CCTTCTCCTGCTGCAGTCAGCACACCCCTGGAGAACACCTGGCTCAGGGTGCATCGAGGCTG  
CAAGTCCTGCAGGCCAACTCACCTGGGTCCCGTCAGCCATGAGCACTTGCTGCAGCGGGT  
AGACAACTTCACTCAGAACCCAGGGATGTTCAGAATCAAAGGTGAACAAAGGCCAGGTC  
TTCAAGGTACAAGGGGCCATGGCATGCCTGGTCCCCCTGGCCGCGGGACCACCTGCT  
GAGAAGGGAGCCAAGGGGCTATGGGACGAGATGGAGCAACAGGCCCTGGGACCCCAAGG  
CCCACCGGGAGTCAAGGGAGAGGCCCTCCAAGGACCCCAGGGTGCCTCAGGGAAAGCAAG  
GAGCCACTGGCACCCCAGGACCCCAAGGAGAGAACGGCAGCAAAGGCATGGGTCTCATT  
GGCCAAAAGGGAAACTGGAACTAAGGGAGAGAAAGGAGACCTGGTCTCCCAGGAAGCAA  
AGGGACAGGGCATGAAAGGAGATGCAGGGTCATGGGCCTCTGGAGGCCAGGGAGTA  
AAGGTGACTTCGGGAGGCCAGGCCACCAGGTTGGCTGGTTCTGGAGCTAAAGGAGAT  
CAAGGACAACCTGGACTGCAGGGTGTCCGGCCCTCCTGGTCAGTGGACACCCAGGTGC  
CAAGGGTGAGCCTGGCAGTGCTGGCTCCCTGGCGAGCAGGACTTCCAGGGAGGCCGGGA  
GTCCAGGAGGCCACAGGCCTGAAAGGAAGCAAAGGGACACAGGACTTCAAGGACAGCAAGGA  
AGAAAAGGAGAACATCAGGAGTCCAGGCCCTGCAGGTGTGAAGGGAGAACAGGGAGGCCAGG  
GCTGGCAGGTCCAAGGGAGGCCCTGGACAAGCTGGCCAGAACAGGGAGACCAGGGAGTGAAAG  
GATCTTCTGGGAGCAAGGAGTAAAGGGAGAAAAGGTGAAAGAGGTGAAAACACTCAGTGTCC  
GTCAGGATTGTCGGCAGTAGTAACCGAGGCCGGCTGAAGTTACTACAGTGGTACCTGGG  
GACAATTGCGATGACGAGTGGCAAATTCTGATGCCATTGTCTCTGCCATGCTGGTT  
ACTCCAAAGGAAGGCCCTGTACAAAGTGGAGCTGGCACTGGCAGATCTGGCTGGATAAT  
GTTCAGTGTGGGAGGCCAGGGAGAGTACCCGTGGAGCTGCAGCGTCTTGACCCGAAACCTTCA  
TGACTGCAGGCCACGAGGAGGACGCAGGCCGGTGCAGCGTCTTGACCCGAAACCTTCA  
CTTCTCTGCTCCGAGGTGTCTCGGCTCATATGTGGGAAGGCAGAGGATCTGTGAGGAGT  
TCCCTGGGACAACGTGAGCAGCCTCTGGAGAGGGGCCATTAATAAGCTAACATCATTGA

## FIGURE 232

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA68886
><subunit 1 of 1, 520 aa, 1 stop
><MW: 52658, pI: 9.16, NX(S/T): 3
MRNKKILKEDELLSETQQAAFHQIAAMEPFEINVPKPKRRNGVNFSLAVVVIYLILLTAGAGL
LVVQLNLQARLRVILEMYFLNDTLAEDSPSFSLQLQSAHPGEHLAQGASRLQVLQAQLTWVR
VSHEHLLQRVDNFTQNPGMFRIKGEQGAPGLQGHKGAMGMPGAPGPPGPPAEKGAKGAMGRD
GATGPSPGPQGPPGVKGEAGLQGPQGAPGKQGATGTPGPQGEKGSKGDGGLIGPKGETGKGE
KGDLGLPGSKDRGMKGDAGVMGPPGAQGSKGFGRPGPGLAGFPGAKGDQGQPGLQGVPG
PPGAVGHPGAKGEPGSAGSPGRAGLPGSPGSPGATGLKGSKGDTGLQGQQGRKGESGVPGPA
GVKGEQGSPGLAGPKGAPQAGQKGDQGVKGSSGEQGVKGEKGERGENSVSRIVGSSNRGR
AEVYYSGTWGTICDDEWQNSDAIVFCRMLGYSKGRALYKVGAGTGQIWLDNVQCRGTESTLW
SCTKNSWGHHDCSVHEEDAGVECSV
```

**Transmembrane domain:**

amino acids 47-66 (type II)

**N-glycosylation sites.**

amino acids 43-47, 83-87, 136-140

**Tyrosine kinase phosphorylation site.**

amino acids 432-440

**N-myristoylation sites.**

amino acids 41-47, 178-184, 253-259, 274-280, 340-346, 346-352,
400-406, 441-447, 475-481, 490-496, 515-521

**Amidation site.**

amino acids 360-364

**Leucine zipper pattern.**

amino acids 56-78

**Speract receptor repeat**

amino acids 422-471, 488-519

**C1q domain proteins.**

amino acids 151-184, 301-334, 316-349

## **FIGURE 233**

CCACCGCGTCCGAAGGCAGACAAAGGTTCATTGTAAGAAGCTCCTCCAGCACCTCCTCT  
CTTCTCCTTTGCCAAACTACCCAGTGAGTGTGAGCATTAAAGAACATCCTCTGCCAAG  
ACCAAAAGGAAAGAAGAAAAAGGGCAAAGC~~AAAATGAA~~ACTGATGGTACTTGTTCAC  
CATTGGGCTAACCTTGCTGCTAGGAGTTCAAGCCATGCCTGCAAATGCCTCTCTGCTACA  
GAAAGATACTAAAAGATCACAACACTGTACAACCTTCCGGAAAGGAGTAGCTGACCTGACACAG  
ATTGATGTCAATGTCCAGGATCATTCTGGATGGGAAGGGATGTGAGATGATCTGTTACTG  
CAAACCCAGCGAATTGCTCTGCTGCCAAAGACGTTTCTTGACCAAAGATCTCTTCG  
TGATTCCCTGCAACAATCAATTGAGAATCTTCATGTATTCTGGAGAACACCATTCTGATTTC  
CCACAAACTGCACTACATCAGTATAACTGCATTCTAGTTCTATATAGTGCAATAGAGCAT  
AGATTCTATAAAATTCTTACTTGTCTAAGACAAGTAAATCTGTGTTAAACAAGTAGTAATAAA  
AGTTAATTCAATCTAAAAAAAAAAAAAA

## **FIGURE 234**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52758
<subunit 1 of 1, 98 aa, 1 stop
<MW: 11081, pI: 6.68, NX(S/T): 1
MKLMVLVFTIGLTLLGVQAMPANRLSCYRKILKDHNCHNLPEGVADLTQIDVNQDHFWDG
KGCEMICYCNFSELLCCPKDVFFGPKISFVIPCNNQ
```

**Important features:**

**Signal peptide:**

amino acids 1-20

**N-glycosylation site.**

amino acids 72-76

**Tyrosine kinase phosphorylation site.**

amino acids 63-71

## **FIGURE 235**

CCACCGCGTCCGCGGACCGCTGGACCCCAGGTCTGGAGCGAATTCCAGCCTGCAGGG  
CTGATAAGCGAGGCATTAGTGAGATTGAGAGAGACTTTACCCCGCGTGGTGGTGGAGGGC  
GCGCAGTAGAGCAGCACAGCGCGGGTCCCGGGAGGCCGCGCTGCTCGCAGCGAG**ATG**  
TGGAAATCTCCTTCACGAAACCGACTCGGCTGTGGCCACCGCGCCGCCCGCGTGGCTGTG  
CGCTGGGGCGCTGGTGTGGCGCTTCTTCTCCTCGGCTCCTCTCGGGTGGTTTA  
TAAAATCCTCCAATGAAGCTACTAACATTACTCAAAGCATATAATGAAAGCATTGGAT  
GAATTGAAAGCTGAGAACATCAAGAAGTTCTTACATAATTACAGATAACCACATTAGC  
AGGAACAGAACAAAACCTTCAGCTGCAAAGCAAATTCAATCCAGTGGAAAGAATTGGCC  
TGGATTCTGTTGAGCTAGCTCATTATGATGTCCTGTTGTCCTACCCAAATAAGACTCATCCC  
AACTACATCTCAATAATTAAATGAAGATGGAAATGAGATTTCACACATCATTATTGAACC  
ACCTCCTCCAGGATATGAAAATGTTCGGATATTGTACCACTTCAGTGTCTCTCCTC  
AAGGAATGCCAGAGGGCGATCTAGTGATGTTAACTATGCACGAAGACTGAAGACTTCTTAAA  
TTGGAACGGGACATGAAAATCAATTGCTCTGGAAAATTGTAATTGCCAGATATGGAAAGT  
TTTCAGAGGAAATAAGGTTAAAATGCCAGCTGGCAGGGCCAAGGGAGTCATTCTACT  
CCGACCCCTGCTGACTACTTGTCTCTGGGTGAAGTCCTATCCAGACGGTGGAACTTCT  
GGAGGTGGTGTCCAGCGTGGAAATATCCTAAATCTGAATGGTGCAGGAGACCCCTCACACC  
AGGTTACCCAGCAAATGAATATGTTAGCGTGGAAATTGCAGAGGCTGTTGGTCTTCAA  
GTATTCTGTTATCCAATTGGATACTATGATGCACAGAAGCTCTAGAAAAAATGGTGGC  
TCAGCACCAACCAGATAGCAGCTGGAGAGGAAGTCTCAAAGTGCCTACAATGTTGGACCTGG  
CTTACTGAAACTTTCTACACAAAAGTCAGATGCACATCCACTCTACCAATGAAGTGA  
CGAGAATTACAATGTGATAGGTACTCTCAGAGGAGCAGTGGAAACCAGACAGATATGTCATT  
CTGGGAGGTCAACGGGACTCATGGGTGTTGGTATTGACCTCAGAGTGGAGCAGCTGT  
TGTTCATGAAATTGTGAGGAGCTTGGAAACACTGAAAAAGGAAGGGTGGAGACCTAGAAGAA  
CAATTGTTGTTGCAAGCTGGATGCAGAAGAATTGGTCTTGGTCTACTGAGTGGCA  
GAGGAGAATTCAAGACTCCTCAAGAGCGTGGCGTGGCTTATATTAAATGCTGACTCATCTAT  
AGAAGGAAACTACACTCTGAGAGTTGATTGTACACCGCTGATGTACAGCTGGTACACAACC  
TAACAAAAGAGCTGAAAAGCCCTGATGAAGGCTTGAAGGCAAATCTTTATGAAAGTTGG  
ACTAAAAAAAGTCCTCCCCAGAGTTCACTGGCATGCCAGGATAAGCAAATTGGATCTGG  
AAATGATTGAGGTGTTCTCCAACGACTTGAATTGCTTCAGGCAGAGCACGGTATACTA  
AAAATTGGAAACAAACAAATTCACTGGCTATCCACTGTATCACAGTGTATGAAACATAT  
GAGTTGGTGGAAAAGTTTATGATCCAATGTTAAATATCACCTCACTGTGGCCAGGTTG  
AGGAGGGATGGTGTGAGCTAGCCAATTCCATAGTGCTCCCTTGATTGTCAGGATTATG  
CTGTAGTTAAGAAAGTATGCTGACAAAATCTACAGTATTCTATGAAACATCCACAGGAA  
ATGAAGACATACAGTGTATCTGATTCACTTTCTGAGTAAAGAATTTCAGGAAAT  
TGCTTCCAAGTTCACTGAGAGACTCCAGGACTTGAACAAAGCAACCCAAATAGTATTAAGAA  
TGATGAATGATCAACTCATGTTCTGAAAGAGCATTATTGATCCATTAGGTTACAGAC  
AGGCCTTTTATAGGCATGTCATCTATGCTCCAAGCAGCCACAACAAGTATGCAGGGAGTC  
ATTCCCAGGAATTATGATGCTCTGTTGATATTGAAAGCAAAGTGGACCCCTCCAAGGCCT  
GGGGAGAAGTGAAGAGACAGATTATGTTGCAGCCTCACAGTGCAGGCAGCTGCAGAGACT  
TTGAGTGAAGTAGCCTAAGAGGATTAGAGAATCCGTATTGAATTGTTGTGGTATGTCA  
CTCAGAAAGAATCGTAATGGGTATATTGATAAATTAAAATTGGTATATTGAAATAAGT  
TGAATATTATATAA

## **FIGURE 236**

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA52756
><subunit 1 of 1, 750 aa, 1 stop
><MW: 84305, pI: 6.93, NX(S/T): 10
MWNLHETDSAVATARRPRWLCA GALVLAGGFFLLGFLFGWFIKSSNEATNITPKHNMK AFL
DELKAENIKKFLHNFTQIPIHLAGTEQNFQLAKQIQSQWKEFGLDSVELAHYDVLLSYPNKTH
PNYISIINEDGNEIFNTSLFEPPPPGYENVSDIVPPFSAFSPQGMPEGDLVYVNYARTEDFF
KLERDMKINC SGKIVIARYGKVFRGNKVKN AQLAGAKGVILYSDPADYFAPGVKSYPDGWNL
PGGGVQRGNILNLNGAGDPLTPGY PAN EYAYRRGIAEAVGLPSIPVHPIGYYDAQKLLEKMG
GSAPPDSSWRGSLKVPYNVGP GFTGNFSTQVKMHIHSTNEVTRIYNVIGTLRGAVEPD RYV
ILGGHRDSWVFGGIDPQSGAAVVHEIVRSFGTLKKEGWRPRRTILFASWDAEEFGLLGSTE W
AEENSRLLQERGVAYINADSSIEGNYTLRV DCTPLMYSLVHNLT KELKSPDEGFEGKSLYES
WTKKSPSPEFSGMPRI SKLGS GND FEV FFQRLGIASGRARYTKNWETNKFSGYPLYHSV YET
YELVEKFYDPMFKYH LTVAQVRGGMV FELANSIVLPFDCRDYAVVLRKYADKIYSISMKH PQ
EMKTYSVSFDSLFS AVKNFT EIASKF SERLQDFDKSNP IVL RMMNDQLMFLERA FIDPLGLP
DRPFYRHVIYAPSSH NKYAGESFP GIYDALFDIESKVDP SKAWGEVKRQIYVAAFTVQAAA E
TLSEVA
```

**Signal sequence:**

amino acids 1-40

**N-glycosylation sites.**

amino acids 76-80, 121-125, 140-144, 153-157, 195-199, 336-340,  
459-463, 476-480, 638-642

**Tyrosine kinase phosphorylation sites.**

amino acids 363-372, 605-613, 606-613, 617-626

**N-myristoylation sites.**

amino acids 85-91, 168-174, 252-258, 256-262, 282-288, 335-341,  
360-366, 427-433, 529-535, 707-713